

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 16:52:01 ; Search time 4299 Seconds

(without alignments)
2530.037 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230

Sequence: 1 MASLGLQVLYLGLGLG.....PGPPKVKSEFNSYSUTGV 230

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9045947

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-INITs-bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
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-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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14: gb_vi:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	230	100.0	693	6	CQ732222 Sequence
2	230	100.0	693	2	AF250558 Homo sapi
3	230	100.0	1400	6	AR340765 Sequence
4	230	100.0	1400	6	BD085944 Elongatio

5	230	100.0	1475	6	AX092348 Sequence
6	230	100.0	1475	6	AX299996 Sequence
7	230	100.0	1475	6	AX395213 Sequence
8	230	100.0	1475	6	AX454606 Sequence
9	230	100.0	1475	6	AX464358 Sequence
10	230	100.0	1475	6	AX491084 Sequence
11	230	100.0	1475	6	AX697065 Sequence
12	230	100.0	1475	6	AX358474 Homo sapi
13	230	100.0	1506	9	BC014424 Homo sapi
14	230	100.0	1518	9	BC071747 Homo sapi
15	230	100.0	1918	9	AF177340 Homo sapi
16	230	100.0	2742	6	BD237562 Membrane-
17	230	100.0	2863	6	AX136129 Sequence
18	230	100.0	2863	6	BD123517 Secretary
19	230	100.0	2863	9	AK075371 Homo sapi
20	230	100.0	2959	9	AK075405 Homo sapi
21	230	100.0	109465	9	AL158821 Human DNA
22	186	80.9	1441	6	AX286822 Sequence
23	131	57.0	693	6	AX497200 Sequence
24	127	55.2	1524	6	AR340718 Sequence
25	127	55.2	1524	6	BD085897 Elongatio
26	67	29.1	615	6	AX136475 Sequence
27	67	29.1	615	6	BD123715 Secretary
28	59	25.7	1032	4	AB115779 Bos tauru
29	58	25.2	779	6	AX286824 Sequence
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32	58	25.2	953	4	AF358907 Canis fam
33	58	25.2	2828	10	BC015252 Mus muscu
34	58	25.2	184872	10	AL672243 Mouse DNA
35	58	25.2	239385	2	AC109686 Rattus no
36	58	25.2	250600	2	AC136646 Rattus no
37	58	25.2	268828	2	AC091513 Rattus no
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39	56	24.3	405	6	BD077679 5'EST of
40	55	23.9	324	6	AX939253 Sequence
41	55	23.9	324	6	BD077680 5'EST of
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43	36	15.7	182	6	AX072760 Sequence
44	31	13.5	49323	2	AC107455 Mus muscu
45	16	7.0	51	6	AX165469 Sequence

ALIGNMENTS

RESULT 1
LOCUS CQ732222 693 bp DNA
DEFINITION Sequence 18156 from Patent WO02068579.
ACCESSION CQ732222
VERSION CQ732222.1 GI:42311107
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 18156 06-SEP-2002;
PE Corporation
FEATURES
source
1..693
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ORIGIN

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Pred. No.: 230.00 Matches: 230

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x CQ732222 (1-693)

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 Db 1 ATGGCCCTCTTGCCCTCCAACTTGCGGCTACATCTAGCCCTTCTGGGGCTTTGGGC 60
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
 Db 61 ACATGGTTCCTGCTGCTGCTCCAGCTGGAAACAAATCTTATGTCGGTGCCAGCAT 120
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
 Db 121 GTGACAGCATGGCTTCTCCAGGGCTCTGATGGAAATGGCCACACAGCAGCAGGC 180
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 Db 181 ATCAACCAGTGTACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 240
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 241 CAGGCCATGATGGATGATCATCAGTCAATCTCTCCCTGGGCTGCAATTCTCTGTG 300
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAla 120
 Db 301 GGCGATGATGACACAGTCTTCTCCAGAAATCCGACCAAGACAGATGGCGGTGCA 360
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 361 GGATGAGCTTTTTCATCTTGGAGGCTCTCTGGATTCATCTCTGCTGGAACTT 420
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 160
 Db 421 CATGGGATCTACGGGACTTCTACTCACACTGGTGCCTGACAGCATGAATTTGAAATT 480
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 481 GAGAGGCTCTTATCTTGGGATTAATTTCTCTCTCTCTGATGAGCTGGAAATATC 540
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 541 CTCTGCTTTCTGCTCATCTCCAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 600
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValLysSerGlu 220
 Db 601 CAACCTCTGCCCAAGAGACTCTCCAAAGCCTGTCAACTCCCAAGTCAGAGATGAG 660
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 661 TTCATTTCTTACAGCTGACAGGATATGTG 690

RESULT 2
 AF250558 693 bp mRNA linear PRI 10-JUN-2002
 LOCUS Homo sapiens claudin-2 mRNA, complete cds.
 DEFINITION AF250558
 ACCESSION AF250558.1 GI:9755008
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS Sakaguchi, T., Gu, X., Golden, H.M., Suh, E., Rhoads, D.B. and
 TITLE Cloning of the human claudin-2 5'-flanking region revealed a
 TATA-less promoter with conserved binding sites in mouse and human
 factor-1alpha

JOURNAL J. Biol. Chem. 277 (24), 21361-21370 (2002)
 MEDLINE 22050612
 PUBMED 11934881
 REFERENCE 2 (pages 1 to 693)
 AUTHORS Sakaguchi, T., Gu, X., Golden, H.M., Suh, E., Rhoads, D.B.,
 TITLE Direct Submission
 JOURNAL Submitted (30-MAR-2000) Gastrointestinal Unit, Massachusetts
 General Hospital, Fruit Street, Boston, MA 02114, USA
 FEATURES
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 1.693
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 GEALYGIITISLPSLILAGIILCPSCSGQNRNSVYDAQAPLATRSPRPQPKVK
 SEFNSISLGLGY"

ORIGIN
 Alignment Scores:
 Pred. No.: 2,12e-238 Length: 693
 Score: 230.00 Matches: 230
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

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 Db 1 ATGGCCCTCTTGCCCTCCAACTTGCGGCTACATCTAGCCCTTCTGGGGCTTTGGGC 60
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
 Db 61 ACATGGTTCCTGCTGCTGCTCCAGCTGGAAACAAATCTTATGTCGGTGCCAGCAT 120
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
 Db 121 GTGACAGCATGGCTTCTCCAGGGCTCTGATGGAAATGGCCACACAGCAGCAGGC 180
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 Db 181 ATCAACCAGTGTACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 240
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 241 CAGGCCATGATGGATGATCATCAGTCAATCTCTCCCTGGGCTGCAATTCTCTGTG 300
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAla 120
 Db 301 GGCGATGATGACACAGTCTTCTCCAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 360
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 361 GGATGAGCTTTTTCATCTTGGAGGCTCTCTGGATTCATCTCTGCTGGAACTT 420
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 160
 Db 421 CATGGGATCTTACGGGACTTCTACTCACACTGGTGCCTGACAGCATGAATTTGAAATT 480
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180

Db 481 GGAGAGCTTTACTGGGCAATATTTCTTCCCTGTTCCCGAGAGCTGGAAATATC 540
Qy 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyTyAspAlaTyGlnAla 200
Db 541 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTACATGCTTACCAAGCC 600
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 601 CAACCTCTTCCCAAGAGCTCTCCAAAGGCTGTGCTCAACCTCCCAAGTCAGAGTGAAG 660
Qy 221 PheAsnSerTySerLeuThrGlyTyTyVal 230
Db 661 TTCAATTCTACAGCTGACAGGATATGTG 690
RESULT 3
AR340765 1400 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 139 from patent US 6573068.
DEFINITION AR340765
ACCESSION AR340765
VERSION AR340765.1 GI:33732507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1400)
AUTHORS Milne Edwards,J.-B.D., Ducleert,A. and Bougueleret,L.
TITLES Claudin-50 protein
JOURNAL Patent: US 6573068-A 139 03-JUN-2003;
FEATURES
source 1..1400
/organism="unknown"
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ORIGIN
Alignment Scores:
Pred. No.: 4,34e-238 Length: 1400
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Qy 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerSerTyTyAlaGlyAlaSerTlle 40
Db 96 ACACGTGTTCCAGTGCCTGCCAGCTCCAGCGAAACAAATCTTATATGTCGGGCGCAGCATT 155
Qy 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrLysSerThrGly 60
Db 156 GTACACACAGTTGGCTTCTCCAGAGGCTCTGGATGGAAATGTGCACACACAGACAGGC 215
Qy 61 TlleThrGlnCysAspLysTySerThrLeuLeuGlyLeuProAlaAspLleGlnAlaAla 80
Db 216 ATCAACCAGTGTGACATCTATAGCACCCCTTCTGGGCTGCCGCGTGACATCCAGGCTGCC 275
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Db 276 CAGGCCATGATGGGACATCCAGTGCATCTCCCTCTGGGCTGTCATTAATCTCTGTGTG 335
Qy 101 GlyMetArgCysThrValPheCysGlnLysSerArgAlaLysAspArgValAlaValAla 120
Db 336 GGCATGAGATGCACAGCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCA 395
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaATrPAsnLeu 140
Db 396 GGTGAGACTTTTTCATCTTGAAGGCTCTCGGATTCATCTCTGTGCTGGAATCTT 455

Qy 141 HisGlyLeuLeuArgAspPheTySerProLeuValProAspSerMetLysPheGlnIle 160
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Db 516 GGAGAGCTTTTACTTGGGCAATATTTCTTCCCTGTCTCCCTGATAGCTGAAATCATC 575
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Db 636 CAACCTCTTCCCAAGAGCTCTCCAAAGGCTGTGCTCAACCTCCCAAGTCAGAGTGAAG 695
Qy 221 PheAsnSerTySerLeuThrGlyTyTyVal 230
Db 696 TTCAATTCTACAGCTGACAGGATATGTG 725
RESULT 4
BD085944 1400 bp DNA linear PAT 27-AUG-2002
LOCUS Elongation CDNA of secretory protein.
DEFINITION BD085944
ACCESSION BD085944
VERSION BD085944.1 GI:22631554
KEYWORDS JP 2001523453-A/86.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1400)
AUTHORS Bougueleret,L., Ducleert,A. and Edwards,J.B.D.M.
TITLES Elongation CDNA of secretory protein
JOURNAL Patent: JP 2001523453-A 86 27-NOV-2001;
GENSET
OS Homo sapiens (human)
PN JP 2001523453-A/86
PD 27-NOV-2001
PR 13-NOV-1998 JP 2000521191
PR 13-NOV-1997 US 60/066677,17-DEC-1997 US 60/069957 PR
09-FEB-1998 US 60/074121,13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116,04-SEP-1998 US 60/099273 PI LYDIE
BOUGUELERET,AYMERIC DUCLEERT,JEAN BAPTISTE DOMAS MILNE PI EDWARDS
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C12N1/21,
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Von Heijne matrix
CC score 5.68999980926514
CC seq ILGLDLGLTVLVA/ML
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Alignment Scores:
Pred. No.: 4,34e-238 Length: 1400
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyTyTlleLeuGlyLeuLeuGlyLeuLeuGly 20

Db 36 ATGGCCTCTTGGCCTCAACTGTGGGCTACACTAGGCTTCTGGGCTTTGGGC 95
 Qy 21 ThrleuValAlaMetleuLeuProSerTrpLysThrSerSerTrpValAlaSerIle 40
 Db 96 ACACGTGGTGGCAGCTGCTCCAGCTGGAACAAAGTTCTTATGTCGGGCGCAGCAT 155
 Qy 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
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 Qy 61 IleThrGlnCysAspIleTrpSerThrleuGlnGlyLeuProAlaAspIleGlnAlaAla 80
 Db 216 ATCACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCCCGCTGACATCCAGGCTGCC 275
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 Qy 101 GlyMetArgCysThrValPheCysGlnGlnuSerArgAlaLysAspArgValAlaAla 120
 Db 336 GGCATGAGATGCACAGCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCA 395
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 Db 396 GGTGAGCTCTTTTCACTCTTGAGGCTCTCGGATTCATTCCTGTTGCTGGAACTCT 455
 Qy 141 HisGlyIleLeuArgAspPheTrpSerProleuValProAspSerMetLysPheGluIle 160
 Db 456 CATGGAGATCTTACGAGACTTCTACTCACCTGAGCTGCTGACACAGAAATTTGAGATT 515
 Qy 161 GlyIleAlaLeuTrpLeuGlyIleIleSerSerleuPheSerleuIleAlaGlyIleIle 180
 Db 516 GGAAGAGCTCTTACTCTGGCATTTCTTCCCTGTTCTCCGATAGCTGGAAATCATC 575
 Qy 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerSerTrpTrpAspAlaTrpGlnAla 200
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 Qy 201 GlnProleuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
 Db 636 CAACCTCTTGCACAGAGGCTCTCCAGGCTGTCAACTCCCAAGATCAAGAGTAG 695
 Qy 221 PheAsnSerTrpSerLeuThrGlyTrpVal 230
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 RESULT 5
 AX092348 1475 bp DNA linear PAT 21-MAR-2001
 LOCUS Sequence 79 from Patent WO0116318.
 DEFINITION AX092348
 ACCESSION AX092348
 VERSION AX092348.1 GI:13444488
 KEYWORDS
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Baton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
 Wood,W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Parent: WO 0116318-A 79 08-MAR-2001;
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 ORIGIN
 Alignment Scores:

Pred. No.: 4,57e-238 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-787-677a-3 (1-230) x AX092348 (1-1475)
 Qy 1 MetAlaSerleuGlyLeuGlnleuValGlyTrpIleleuGlyleuLeuGlyleuLeuGly 20
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 Qy 21 ThrleuValAlaMetleuLeuProSerTrpLysThrSerSerTrpValAlaSerIle 40
 Db 182 ACACGTGGTGGCAGCTGCTCCAGCTGGAACAAAGTTCTTATGTCGGGCGCAGCAT 241
 Qy 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 Db 242 GTGACACAGCTGGCTTCTCCAGAGGCTCTCGATGAGATGTCCACACACAGCAGCAGC 301
 Qy 61 IleThrGlnCysAspIleTrpSerThrleuGlnGlyLeuProAlaAspIleGlnAlaAla 80
 Db 302 ATCACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCCCGCTGACATCCAGGCTGCC 361
 Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerValVal 100
 Db 362 CAGGCCATGATGGAGACATCCAGGCAATCTCTCCCTGGGCTGCATTTATCTGTGGTG 421
 Qy 101 GlyMetArgCysThrValPheCysGlnGlnuSerArgAlaLysAspArgValAlaAla 120
 Db 422 GGCATGAGATGCACAGCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCA 481
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 Qy 161 GlyIleAlaLeuTrpLeuGlyIleIleSerSerleuPheSerleuIleAlaGlyIleIle 180
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 Qy 221 PheAsnSerTrpSerLeuThrGlyTrpVal 230
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 RESULT 6
 AX299996 1475 bp DNA linear PAT 26-NOV-2001
 LOCUS Sequence 1 from Patent WO0166740.
 DEFINITION AX299996
 ACCESSION AX299996
 VERSION AX299996.1 GI:17129473
 KEYWORDS
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 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Baton,D.L., Fong,S., Goddard,A., Godowski,P.J., Grimaldi,C.J.,
 Gurney,A.L., Tumas,D., Watanabe,C.K., Wood,W.I. and Zhang,Z.
 TITLE Compositions and methods for the treatment of immune related
 diseases

JOURNAL Patent: WO 0166740-A 1 13-SEP-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1..1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 4.57e-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x AX299996 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 122 ATGGCCCTCTTGCCCTTCACTTGCGGCTACATCTAGGCTTCTGGGGCTTTTGCGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerSerTyrValGlyAlaSerIle 40
Db 182 ACACGTGGTCCATGCTGCTCCCACTGGAACAAAGTTCTTATGTCGGTCCAGCATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 242 GTACAGACAGATGGCTTCTCCAGAGGCTCTGATGATGATGCCACACAGACAGAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
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QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
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QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db 422 GGCATGATGACACAGCTCTTCTGCGAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 481
QY 121 GlyGlyValAlaPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaIlePheLeu 140
Db 482 GGTGGAGCTTTTTCATCTTGAGGCTCTCTGGGATTCATCTCTGTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGATCTTACGGGACTTCTACTCACACTGGTGGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GAGAGGCTCTTACTTACCTGGCATTAATTTCTCCCTGTTCTCCGATAGCTGAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTGCTCATCTCCAGAGAAATCGCTCAACTACATGATGCTTCAAGACC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValIleValSerGlu 220
Db 722 CAACCTCTTCCACAGAGAGCTCTCCAAAGGCTGTGCAACTCCCAAGTCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCAATTCCTACAGCTGACAGGGTATGTG 811

RESULT 7
AX395213 1475 bp DNA linear PAT 18-MAY-2002
LOCUS Sequence 1 from Patent WO0216429.
DEFINITION AX395213
ACCESSION AX395213.1 GI:21066244
VERSION

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Goddard, A., Goddard, P.J., Gurney, A.L., Hillan, K.J., Polakis, P., Smith, V., Wood, W.T., Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216429-A 1 28-FEB-2002;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1..1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 4.57e-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x AX395213 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 122 ATGGCCCTCTTGCCCTTCACTTGCGGCTACATCTAGGCTTCTGGGGCTTTTGCGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerSerTyrValGlyAlaSerIle 40
Db 182 ACACGTGGTCCATGCTGCTCCCACTGGAACAAAGTTCTTATGTCGGTCCAGCATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 242 GTACAGACAGATGGCTTCTCCAGAGGCTCTGATGATGATGCCACACAGACAGAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCCAGGTGACATCTATAGACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCCATGATGTGACATCATGCAATCTCTCCCTGGCTGCTGATTAATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db 422 GGCATGATGACACAGCTCTTCTGCGAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA 481
QY 121 GlyGlyValAlaPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaIlePheLeu 140
Db 482 GGTGGAGCTTTTTCATCTTGAGGCTCTCTGGGATTCATCTCTGTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGATCTTACGGGACTTCTACTCACACTGGTGGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GAGAGGCTCTTACTTACCTGGCATTAATTTCTCCCTGTTCTCCGATAGCTGAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTGCTCATCTCCAGAGAAATCGCTCAACTACATGATGCTTCAAGACC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValIleValSerGlu 220
Db 722 CAACCTCTTCCACAGAGAGCTCTCCAAAGGCTGTGCAACTCCCAAGTCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230

Db 782 TTCATTCTACAGCTGACAGGGTATGTG 811

|||||

RESULT 8
AX454606 1475 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 191 from Patent WO0208284.
DEFINITION AX454606
ACCESSION AX454606
VERSION AX454606.1 GI:21713927
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerltzen, M.E., Goddard, A.,
Goddard, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLES Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 191 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerltzen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES
source 1. 1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 4.57e-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x AX454606 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCTCTCTTGGCTTCACTGTGGCTACATCTTGGCTTGGCTTGGCTTGGCT 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValAlaSerIle 40
Db 182 ACATGTGTTGCCATGCTGCTCCCAAGCTGGAACAACTTCTTATGTCGGCCAGCAT 241

QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGTTGGCTTCTCCAGGGCTCTGATGAAATGGCACACACAGCAGGC 301

QY 61 IleThrGlnCysAapIleTyrSerThrLeuLeuGlyLeuProAlaAapIleGlnAla 80
Db 302 ATCAACCCAGTGTGATCTATAGCACCTTCTGGGCTGCGCTGATCATCAGGCTGCC 361

QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGTGACATCCAGTGCAATCTCTCCCTGGGCTGATTAATCTGTGTG 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAspArgValAlaValAla 120
Db 422 GGCATGATGATCACAAGTCTTCTGCCAGGAATCCGAGCAGAAAGACAGTGGCGTGA 481

QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
Db 482 GGTGGAGTCTTTTTCATCTCTTGAGGCTCTCTGGGATTCATTCGTGGCTGGAATCTT 541

QY 141 HisGlyIleLeuArgAapPheTyrSerProLeuValProAapSerMetLysPheGluIle 160
Db 542 CATGGATCTCTACGGGACTTCTACTCACCACTGTGCTACAGCAGCAATTTGACATT 601

QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 602 GGAAGAGCTCTTACTTGGGCTGATTAATTTCTCCCTGTTCTCCGATAGCTGGATCATC 661

QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerSerTyrTyrAapAlaTyrGlnAla 200
Db 662 CTGTGCTTTCCTGCTCATCCAGAGAAATGCTCCCACTACATGATGCTTCCAAAGCC 721

QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValIlySerGlu 220
Db 722 CAACCTTTCGCCACAGGACTCTCCAGGCTGTGTCACTCCCAAGTCAGAGTGTG 781

QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATTCTACAGCTGACAGGGTATGTG 811

RESULT 9
AX464358 1475 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 491 from Patent WO0140466.
DEFINITION AX464358
ACCESSION AX464358
VERSION AX464358.1 GI:21899195
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerltzen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tuma, D., Watanabe, C.K.,
Wood, W.I., and Zhang, Z.
TITLES Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 491 07-JUN-2001;
Genentech Inc. (US)

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source 1. 1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 4.57e-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x AX464358 (1-1475)

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Db 122 ATGGCTCTCTTGGCTTCACTGTGGCTACATCTTGGCTTGGCTTGGCTTGGCT 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValAlaSerIle 40
Db 182 ACATGTGTTGCCATGCTGCTCCCAAGCTGGAACAACTTCTTATGTCGGCCAGCAT 241

QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGTTGGCTTCTCCAGGGCTCTGATGAAATGGCACACACAGCAGGC 301

QY 61 IleThrGlnCysAapIleTyrSerThrLeuLeuGlyLeuProAlaAapIleGlnAla 80
Db 302 ATCAACCCAGTGTGATCTATAGCACCTTCTGGGCTGCGCTGATCATCAGGCTGCC 361

OY		81	GlnAlamctmValThSerserlalleSerSerleuaAlyeIlelseerVal	100
Dd		362	CAGGCGATGAATGGTACATCCAGTCGATCTCTCCTGGCTGCATTAATCTGTGGTG	421
OY		101	GlyMetarqCyethrValPheCysgInguSerArgalalyeAsparValAlaValAla	120
Dd		422	GGCATGATGACACAGTCTTCTGCCAGAAATCCGACCAAGAACAAGACAGATGGCGGTAGCA	481
OY		121	GlyglyValAlphepheIleLeuglyglyLeuleuglyPheIleProvalAlatrpAsnleu	140
Dd		482	GGTAGAGCTTTTTCATCTTGGAGGCTCTCCGGGATTCATTCTGTTGCCGGAATCTT	541
OY		141	HiseglyIleLeuarXAspPhetyrSerProleuValProaspSerMetLysphegluile	160
Dd		542	CATGGGATCTCACGGGACTTCTACTCACCACTGAGCTGTACAGCATGAATTTAGATT	601
OY		161	GlyglualaleTyrlleuglyIlelleseSerleupeSerleuIlealaglylleile	180
Dd		602	GGAGAGGCTCTTACTTGGGCAATTTCTTCTCCGTTCCTCCTGATAGCTGAATCATC	661
OY		181	LeucySpheSerCySeSerSerGlharGaenaAgSerarTYrrTYraSPallayrolala	200
Dd		662	CTGTGCTTTTCTGTCTCATCCAGAGAAATCCCTCAACTPAAGATGCCATCACAGGC	721
OY		201	GlnProleuaIaThrArgSerSerProargProglyGlnInproProLyValIlysSerGu	220
Dd		722	CAACTCTTGGCCACAGAGAGCTCTCCMAAGCCTGTGTCACTCCCAAAGTCAAGATG	781
OY		221	PheaenSerTYrSerleuThrglyTYrVal	230
Dd		782	TTCATTTCTTACAGCCTGACAGGGATGTGG	811
RESULT 10				
AX491084				
LOCUS	AX491084	1475 bp	DNA	linear
DEFINITION	Sequence 191 from Patent WO0200690.			PAT 16-AUG-2007
ACCESSION	AX491084			
VERSION	AX491084.1	GI:22323879		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Baker,K.P., Ferrara,N., Gebler,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Masters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.			
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis			
JOURNAL	Patent: WO 0200690-A 191 03-JUN-2002;			
FEATURES				
source	Location/Qualifiers 1..1475 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"			
ORIGIN				
Alignment Scores:				
Pred. No.:	4.57e-238	Length:	1475	
Score:	230.00	Matches:	230	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	6	Gaps:	0	
US-09-787-677A-3 (1-230) x AX491084 (1-1475)				
OY		1	MetaIlaSerleuGlyLeuGlnleuValaGlyTYrIleleuGlyLeuLeuGlyleuGly	20
Dd		122	ATGGGCTCTCTGGGCTCCAACTTGtGGGCTACATCTTAAGGCTTCTGggGCTTGTGGGC	181

OY	21	ThiruVala1a1aMetLeuLeuProSeTriphThrsSerSerTyrrVala1a1aSerIle	40
Db	182	ACACTGGTGGCAATGCTGCTCCACAGCTGAAAAACAAGTTCTTATGTCGGTCCAGCAATT	241
OY	41	ValThra1a1aValGlyPheSerTyGlyLeuTrpMetGluCysAlaThrHisSerThGly	60
Db	242	GTGACAGAGATTGGCTTCTCCAAAGGCGCTGTGATGAATGTGTGCACACACAGACAGCG	301
OY	61	IlleThrGlnCysAspIleTyrrSerThLeuLeuGlyLeuProAlaAspIleGlnAlaAla	80
Db	302	ATCCACCAGGTGTGACATCTATAGACACCTTCGTGGCGCTGCCTGTGACATCCAGCGTCC	361
OY	81	GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal	100
Db	362	CAGGCGCATGATGTGACATCCAGTGCATCTCTCCCTGGCGCTGATTAATCTCTGTGTG	421
OY	101	GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIysAspArgVala1a1aVala1a	120
Db	422	GGCATGAGATGCACAGTCTTCTGCGCAGAAATCCGACCAAGACAGATGTGCGGTAGCA	481
OY	121	GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProVala1a1aTrpAsnLeu	140
Db	482	GGTGAAGCTTTTTCATCTTGAGGCGCTCCGTGGATTCATCTCTGTGTGCTGGAAATCTT	541
OY	141	HisGlyIleLeuArgAspPheTyrrSerProLeuValProAspSerMetIysPheGluIle	160
Db	542	CATGGGATCTCAGCGGACTTCTATCTCACACATGTCCTGACAGCAAGAAATTTGAGATT	601
OY	161	GlyGluAlaLeuTyrrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle	180
Db	602	GGAGAGGCTCTTACTGTGGGCAATATTCTTCCCTGTTCTCCGAAAGCTGAGATCATC	661
OY	181	LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrrTrpAspAlaTyrrGlnAla	200
Db	662	CTGTGCTTTTCTCTCTATCCACAAGAAATGCTCCAACTACATGATGCTTACCAAGCC	721
OY	201	GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIysValIysSerGlu	220
Db	722	CAACTCTTGCCACAAAGAGCTCTCCAAGCGCTGTCACTCCCAAAAGTCAAGAGTGTAG	781
OY	221	PheAsnSerTyrrSerLeuThrGlyTyrrVal	230
Db	782	TTCAATTCTCTACAGCTGCACAGGCTATGTG	811
RESULT 11			
AX697065	LOCUS	AX697065	1475 bp DNA linear PAT 02-APR-2003
DEFINITION	Sequence 133 from Patent WO0078961.		
ACCESSION	AX697065		
VERSION	AX697065.1	GI:29498042	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1	Ferrara, N., Stewart, T. A., Williams, P. M., Baker, K. P., Desnoyers, L.,	
AUTHORS	Eaton, D. L., Gao, W. Q., Pan, J., Boetstein, D., Fong, S., Goddard, A.,		
	Gidomaki, P. J., Gurney, A. L., Smith, V., Tumes, D., Wood, W. T.,		
TITLE	Grimaldi, C. J., Hillan, K. J., Paoni, N. F., Roy, M. A. and Watanabe, C. K.		
	Secreted and transmembrane polypeptides and nucleic acids encoding		
	the same		
JOURNAL	Patent: WO 0078961-A 133 28-DEC-2000;		
FEATURES	Genentech Inc. (US)		
source	Location/Qualifiers		
	1..1475		
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ORIGIN	/db_xref="taxon:9606"		
Alignment Scores:			

Pred. No.: 4,576-238 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-787-677a-3 (1-230) x AK697065 (1-1475)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
Db 122 ATGGCTCTCTTGGCTTCCAACTGTGGGCTACATCTCAGGCTTCTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValAlaSerIle 40
Db 182 ACACGTGGTGGCAAGCTGCTCCAGCTGGAAACAACTTATATGTCGGTCCAGCAT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACAGCAGTTGGCTTCTCCAAAGGCTCTGATGATGATGTCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCCAGTGTGACATCTATAGACACCTCTGGGCTGCCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAl 100
Db 362 CAGGCCATGATGGAGACATCCAGTGCATCTCTCCCTGGCTGCATTAATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAspArgValAlaValAla 120
Db 422 GGCAATGATGACACAGCTTCTTGCAGGAATCCCGAGCANAAGACAGTGGCGGTGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrPheLeu 140
Db 482 GGTGAGTCTTTTCATCTCTGGAGGCTCTCGGATTCATCTCTGTTGCTCGAATCTT 541
QY 141 HisGlyIleLeuAspPheTyrSerProLeuValProAspSerMetIlePheGlnIle 160
Db 542 CATGGATCTTACGGGACTTCTACTCACCTGATGCTTGCACAGCATGAATTTGAGATT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGGCTTTTACTTGGGCAATTTCTTCCCTGTTCTCCGATGATGCTGGAATATC 661
QY 181 LeuCySPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTCTCTATCCAGAGAATGCTCCAACTACTACGATGCTTACCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
Db 722 CAACTCTTGGCACAAGAGCTCTCCAGGCTGTGTCACCTCCCAAGTCAAGAGTAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCAATTCCTACAGCTGACAGGATGTG 811
RESULT 12
AY358474 1475 bp mRNA linear PRI 03-OCT-2003
LOCUS Homo sapiens clone DNA64886 Claudin-2 (UNQ705) mRNA, complete cds.
DEFINITION AY358474
ACCESSION AY358474
VERSION AY358474.1 GI:37182070
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1475)
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,

JOURNAL PUBMED 12975309
REFERENCE 2 (bases 1 to 1475)
AUTHORS Clark,H.F.
TITLE Direct Submision
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
Source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA64886"
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122. 814
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ORIGIN
Alignment Scores:
Pred. No.: 4,576-238 Length: 1475
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValAlaSerIle 40
Db 182 ACACGTGGTGGCAAGCTGCTCCAGCTGGAAACAACTTATATGTCGGTCCAGCAT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACAGCAGTTGGCTTCTCCAAAGGCTCTGATGATGATGTCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCCAGTGTGACATCTATAGACACCTCTGGGCTGCCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAl 100
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Db	Accession	Version	Source	Organism	Reference	Authors	Title	Journal	Remark
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Qy	181	LeuCyPheSerCySsSerSerGlnaArgaAaArgSerAaTyTYRAspAlaTYRGlnaIa	200						
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Qy	201	GlnProLeuAlaIaThrArgSerSerProArgProGlyGlnProProGlyValLysSerGlu	220						
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DEFINITION	BC014424								
ACCESSION	BC014424								
VERSION	BC014424.1								
KEYWORDS	MG.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	1 (bases 1 to 1506)								
AUTHORS	Strauberg, R. L., Feingold, B. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Sherman, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Butow, K. H., Schaefer, C. F., Bat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J. J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scherz, T. E., Brownstein, M. J., Usdin, T. B., Toopiyki, S., Cenci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullany, S. J., Bosak, S. A., McSwan, P. J., McMerhan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Morley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hult, S. W., Villalón, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, M. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, G. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butlerfield, Y. S., Krzywinski, M. I., Skalka, U., Smalls, D. E., Scherch, A., Schein, J. E., Jones, S. J. and Marra, M. A.								
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences								
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.								
PUBMED	12477932								
REFERENCES	2 (bases 1 to 1506)								
AUTHORS	Strauberg, R.								
TITLE	Direct Submission								
JOURNAL	Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA								
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov								
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca								

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Tanka Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prahbu, Parvaneh Saeedi, Jr Santos, Angelique Scherch, Ursula Skalska, Duane Smalls, Jeff Stoltz, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNt at: <http://image.llnl.gov>
Series: IRAL Plate: 29 Row: m Column: 11
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Location/Qualifiers

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ORIGIN

Alignment Scores:

Score: 4.67e-238 Length: 1506

Score: 230.00 Matches: 230

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-787-677A-3 (1-230) x BC014424 (1-1506)

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 DEFINITION complete cds.
 ACCESSION BC071747
 VERSION BC071747.1 GI:47938251
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1618)
 Strauberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenman,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhac,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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 Seipleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Uebli,T.B., Tobinlyki,S.,
 Carinici,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,K.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bonifard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalka,U., Smilins,D.E.,
 Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12479932
 2 (bases 1 to 1618)
 Strauberg,R.
 Direct Submission
 Submitted (01-JUN-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovics
 cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-sngc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 57 Row: n Column: 5
 This clone was selected for full length sequencing because it
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 Pred. NO.: 5.03e-238 Length: 1618
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 Query Match: 100.00% Indels: 0
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 Db 508 ATCCACAGTGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGCTGCC 567
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DEFINITION	Homo sapiens clone SP82 claudin 2 mRNA, complete cds.		
ACCESSION	AF177340		
VERSION	AF177340.1	GI:10503979	
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE AUTHORS	1 (bases 1 to 1918) Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qiu,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.		
TITLE	Novel human cDNA clone with function of inhibiting cancer cell growth		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1918) Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qiu,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-AUG-1999) National Laboratory for Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie Tu Road, Shanghai 200032, P.R. China		
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ORIGIN			
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Prod. No.:			

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Job time : 4303 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 16:50:21 ; Search time 497 Seconds
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Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xjh
-O=/cgn2.1/USPRO.spool/US09787677/runat.20122004.132817.19758/app.query.fasta_1.391
-DB=N.GeneSeq.23Sep04 -QPM=fastap -SUFFIX=oli.rng -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oli.go -TRANS=human40.cdt
-LIST=45 -DOCALLIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFM=pic -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09787677 @CGN 1.1 470 @runat.20122004.132817.19758 -NCPU=6 -ICPU=3
-NO.MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPELLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N.GeneSeq.23Sep04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2002bs:*\n8: geneseqn2003as:*\n9: geneseqn2003bs:*\n10: geneseqn2003cs:*\n11: geneseqn2003ds:*\n12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230	100.0	1400	2	AAK97865 Human sec
2	230	100.0	1400	10	ADJ45986 Novel hum
3	230	100.0	1400	12	ADP18800 Human sec
4	230	100.0	1475	3	AAA37060 Human PRO
5	230	100.0	1475	4	AAFS4296 DNA encod
6	230	100.0	1475	4	AAAS21489 Human CDN

7	230	100.0	1475	4	AA515360 cDNA enco
8	230	100.0	1475	4	AAFP2097 Human PRO
9	230	100.0	1475	6	AB574417 Human CDN
10	230	100.0	1475	6	ABL88167 Human PRO
11	230	100.0	1475	6	ABK11089 cDNA enco
12	230	100.0	1475	6	ABL95656 Human ang
13	230	100.0	1475	8	ACA91203 Novel hum
14	230	100.0	1475	8	ACD81580 Human CDN
15	230	100.0	1475	8	ACA60402 Novel hum
16	230	100.0	1475	8	ACA03848 cDNA enco
17	230	100.0	1475	8	ACA58849 cDNA enco
18	230	100.0	1475	8	ABX89386 DNA encod
19	230	100.0	1475	8	ACA4025 cDNA enco
20	230	100.0	1475	8	ACA91289 cDNA enco
21	230	100.0	1475	8	ACD45188 Human sec
22	230	100.0	1475	8	ACD42040 Human sec
23	230	100.0	1475	8	ACA93736 Human CDN
24	230	100.0	1475	8	ACA67310 cDNA enco
25	230	100.0	1475	8	ACH66283 Novel hum
26	230	100.0	1475	8	ACA04269 Human CDN
27	230	100.0	1475	8	ACD02337 Novel hum
28	230	100.0	1475	8	ACA89328 Novel hum
29	230	100.0	1475	8	ACA68965 Novel hum
30	230	100.0	1475	8	ACA98487 Human PRO
31	230	100.0	1475	8	ACA53412 cDNA enco
32	230	100.0	1475	9	ADA46010 Novel hum
33	230	100.0	1475	9	ADA76441 Human PRO
34	230	100.0	1475	9	ADB17136 Human CDN
35	230	100.0	1475	9	ADA19091 Human PRO
36	230	100.0	1475	9	ADA61714 Homo sapi
37	230	100.0	1475	9	ADB19499 Novel hum
38	230	100.0	1475	9	ADB28040 cDNA enco
39	230	100.0	1475	9	ADA86519 Novel hum
40	230	100.0	1475	9	ADB16083 Human PRO
41	230	100.0	1475	9	ADA47869 Human PRO
42	230	100.0	1475	9	ACH03615 Human sec
43	230	100.0	1475	9	ACD68333 Novel hum
44	230	100.0	1475	9	ADA19941 Novel hum
45	230	100.0	1475	9	ADA67664 Human PRO

ALIGNMENTS

RESULT 1	
AAK97865	
ID	AAK97865 standard; cDNA; 1400 BP.
XX	
AC	AAK97865;
XX	
DT	23-SEP-1999 (first entry)
XX	
DE	Human secreted protein encoding cDNA #53.
XX	
KW	Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;
KM	diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09925825-A2.
XX	
PD	27-MAY-1999.
XX	
XX	
PF	13-NOV-1998; 98WO-IB001862.
XX	
PR	13-NOV-1997; 97US-0066677P.
PR	17-DEC-1997; 97US-0069967P.
PR	09-FEB-1998; 98US-0074121P.
PR	13-APR-1998; 98US-0081563P.
PR	10-AUG-1998; 98US-0096116P.
PR	04-SEP-1998; 98US-0099273P.
XX	
PA	(GEST) GENSET.
XX	

PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
 XX WPI: 1999-347472/29.
 DR P-PSDB; AAY36181.
 XX Extended cDNAs encoding secreted proteins.
 XX Claim 1, Page 254-255; 307pp; English.
 CC AAY97813-X97906 represent extended cDNA's which encode novel human
 CC secreted proteins (see AAY36129-Y36222) and which have cytostatic,
 CC thrombotic and osteoplastic activity. The extended cDNAs can be used to
 CC express secreted proteins or parts of them or to obtain antibodies
 CC capable of binding to the secreted proteins. They may also be used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC Uses also include design of expression vectors and secretion vectors.
 XX
 SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.38e-212 Length: 1400
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-09-787-677a-3 (1-230) x AAY97865 (1-1400)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 36 ATGGCTCTCTTGGCTCCCACTGTGGGCTACATCTTAGGCTTCTGGGCTTGGGC 95
 QY 21 ThrIleuValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
 Db 96 ACACCTGGTGGCAAGCTGCTCCCACTGGAAACAACTTCTTATGTCGGTGCACGACATT 155
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 Db 156 GTGACAGACAGTTGGCTTCCAGAGGCTCTGAGATGATGTCACACACACAGCAGC 215
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 216 ATCACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCGTGAATCAGAGCTGCC 275
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 276 CAGGCAATGATGATGACATCCAGTCAATCTCCCTGGCTGATTAATCTGTGTG 335
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
 Db 336 GGCATGAGATGACAGTCTTCTGCCAGAAATCCAGACCAAGACAGAGTGGCGTAGCA 395
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaIleTrpAsnLeu 140
 Db 396 GGTGGAGCTCTTTTCATCTTGGAGGCTCTCGGAGTTCATCTCGTTGCTGGAAATCTT 455
 QY 141 HisGlyIleLeuAlaGAspPheTyrSerProLeuValProAspSerMetIlyPheGluIle 160
 Db 456 CATGGAGATCCACGGAGCTTACTACACACTGGCTGACAGCATGAAATTTGAGATT 515
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuAlaGlyIleIle 180
 Db 516 GGAAGAGCTCTTACTTGGCATTTTCTTCCCTGTTCTCCGATGATGCGAATCTC 575
 QY 181 LeuCyPheSerCysSerSerGlnArgAlaIleSerSerValTyrAspAlaTyrGlnAla 200
 Db 576 CTCGTCTTTCTCTGCTCATCCAGAGAAATGCTCCAACTACTACGATGCCAACAGCC 635
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPheValIlySerGlu 220
 Db 636 CAACTCTTGGCACAGAGGCTCTCCAGGCTGTGTCAACTCCCAAGATCAAGAGTAG 695

QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 696 TTCAATTCCTACAGCCTGACAGGATATGTG 725
 RESULT 2
 ID ADJ45986 standard; cDNA; 1400 BP.
 AC ADJ45986;
 XX 06-MAY-2004 (first entry)
 DT
 XX Novel human secreted protein-related cDNA sequence SeqID139.
 DE
 XX secreted protein; upstream regulator; gene therapy; protein purification;
 KW protein synthesis; chromosomal mapping; individual identification;
 KW forensic; hereditary disease; drug reaction; immunos assay;
 KW epitope mapping; vaccine; immune system regulation;
 KW haematopoietic system; tissue growth; reproductive hormone;
 KW cell migration; blood clotting; receptor/ligand interaction;
 KW adhesion molecule; assisted drug delivery;
 KW human glial maturation factor gamma-2; neurite outgrowth;
 KW neurite resprouting; human; gene; ss.
 XX Homo sapiens.
 XX US2003144490-A1.
 XX 31-JUL-2003.
 XX 10-DEC-2002; 2002US-00319763.
 XX 13-NOV-1997; 97US-0066677P.
 XX 17-DEC-1997; 97US-0069957P.
 XX 09-FEB-1998; 98US-0074121P.
 XX 13-APR-1998; 98US-0081563P.
 XX 10-AUG-1998; 98US-0096116P.
 XX 04-SEP-1998; 98US-0099273P.
 XX 13-NOV-1998; 98US-0019197P.
 XX 15-SEP-2000; 2000US-00663600.
 XX (EDMA/) EDWARDS J D M.
 XX (DUC/L) DUCLERT A.
 XX (BOUG/) BOUGUELERET L.
 XX Edwards JDM, Duclert A, Bougueleret L;
 XX WPI: 2003-851788/79.
 DR P-PSDB; ADJ46033.
 PT New nucleic acid encoding secreted human polypeptides, useful e.g. in
 PT gene therapy or diagnosis, also encoded proteins, potential therapeutic
 PT agents.
 XX Claim 3; SEQ ID NO 139; 269pp; English.
 PS
 XX This invention relates to novel purified isolated polynucleotides which
 CC comprise a sequence that encodes at least 10 amino acids (aa) from any of
 CC 48 secreted polypeptide sequences, given in the specification, or
 CC fragments of polypeptides encoded by human cDNA contained in the
 CC corresponding deposited clone. The DNA sequences of the invention encode
 CC secreted proteins (or their fragments) and can be used to
 CC identify/isolate upstream regulators, potentially useful in gene therapy
 CC or protein purification, by controlling protein synthesis, as probes for
 CC chromosomal mapping, identification of individuals, and for diagnosis or
 CC forensics, for example identifying genes associated with hereditary
 CC diseases or drug reactions, for recombinant expression of the encoded
 CC proteins or, where the DNA sequence encodes a signal peptide, for
 CC directing secretion of heterologous polypeptides. Polypeptides encoded by
 CC the DNA sequences of the invention can be used to raise antibodies,
 CC useful for detecting the polypeptide, as (ant)agonists, or for preparing
 CC anti-idiotypic antibodies, as tags in for example immunoassays, epitope
 CC mapping or vaccines, also as molecular weight markers, to screen for

CC agents with biological activity and as therapeutic agents with
CC potentially a very wide range of activities, for example regulation of
CC the immune or hematopoietic systems, tissue growth, reproductive
CC hormones, cell migration, blood clotting or receptor/ligand interaction,
CC also as adhesion molecules for assisted drug delivery. A typical isolated
CC sequence is human glial maturation factor gamma-2, which stimulates
CC neurite outgrowth and resprouting. The present sequence is a cDNA
CC sequence which encodes a human secreted protein of the invention.

XX Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6,38e-212	Length:	1400
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-787-677A-3 (1-230) x ADP18800 (1-1400)

```
QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
Db 36 ATGGCCCTCTTGCCCTCCAACTGTGGGCTACATCTAGGCTTCTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTrrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 96 ACACTGGTTCCTCACTGCTCCAGCTGGAACCAAGTTCTTATGTCGGTGCAGCATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThGly 60
Db 156 GTGACAGCAAGTTGGCTTCTCCAGAGGCTCTGGATGAAATGTGCACACACAGACAGGC 215
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 216 ATCAACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCCGCTGACATCAGGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 276 CAGGCGCATGATGGAGACATCAGAGCAATCTCCCTGGGCTGCATTAATCTCTGTGGTG 335
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db 336 GGCATGAGATGACACAGCTTCTGCCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCA 395
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaATrPAsnLeu 140
Db 396 GGTGAGACTTTTTCATCTTGGAGGCTCTCGGATTCATCTCTGTGGCTGGAAATCTT 455
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 456 CATGGAGTCTTACCGGAGCTTCTACTCACCACTGGTGGCTGCACACATGAATTTGAGATT 515
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 516 GGAAGAGCTCTTACTTGGGATTAATTTCTCCCTGTTCTCCGATAGCGGAAATATC 575
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 576 CTCTGCTTTTCTGCTCATCTCCAGAAATGCTCCCAACTACTACATGCTTCAAGACC 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 636 CAACCTCTTGCACAAAGAGCTCTCCAAAGGCTGTGCAACTCCCAAGTCAGAGAGTGAG 695
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 696 TTCAATTCTACAGCTGACAGGATATGTG 725
RESULT 3
ID ADP18800 standard; cDNA; 1400 BP.
XX
```

```
AC ADP18800;
XX 26-AUG-2004 (first entry)
DT Human secreted polynucleotide #56.
XX Human secreted polynucleotide #56.
XX Human, secreted protein; gene; ss; genetic disease.
XX Homo sapiens.
XX US2004110939-A1.
XX 10-JUN-2004.
XX 15-OCT-2001; 2001US-00978360.
XX 17-DEC-1998; 98WO-IB002122.
XX 09-FEB-1999; 99WO-IB000282.
XX 21-JUN-2000; 2000WO-IB000951.
XX 15-SEP-2000; 2000US-00663600.
XX (BEST ) GENSET SA.
XX Dumas Milne Edwards J, Bougueleret L, J Robert S, Clusel C;
XX Duclet A;
XX WPI; 2004-440404/41.
XX P-PSDB; ADP19205.
XX New isolated polynucleotide encoding secreted polypeptide, useful for
XX gene therapy, or in diagnostic procedures to identify individuals having
XX genetic diseases resulting from abnormal expression of the genes.
XX Claim 1; SEQ ID NO 56; 113pp; English.
XX The invention relates to human cDNA sequences that encode human secreted
XX proteins. The invention also relates to an antibody that specifically
XX binds to a polypeptide of the invention and a method of binding the
XX polypeptide to an antibody. The polynucleotides are useful for expressing
XX the entire secreted proteins which they encode and for distinguishing
XX human tissues and cells from non-human tissues and cells, and for
XX distinguishing between human tissues and cells that do or do not express
XX the polynucleotides comprising the cDNAs. The polynucleotides and
XX polypeptides are useful in forensic procedures or diagnostic procedures
XX to identify individuals with genetic diseases resulting from abnormal
XX expression of the genes corresponding to the cDNAs. The sequences are
XX also useful in gene therapy to control or treat genetic diseases. This
XX sequence represents a human secreted polynucleotide of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6,38e-212 Length: 1400
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-787-677A-3 (1-230) x ADP18800 (1-1400)
QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
Db 36 ATGGCCCTCTTGCCCTCCAACTGTGGGCTACATCTAGGCTTCTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTrrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 96 ACACTGGTTCCTCACTGCTCCAGCTGGAACCAAGTTCTTATGTCGGTGCAGCATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThGly 60
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Db 156 GTGACAGAGTTGGCTTCCAGAGGCTCTGGATGGATGGATGGACACAGACAGAGC 215
Qy 61 I1ethrGInCYaApI1eTYrSerThIeuleuGlyLeuPFOI1aApI1eGIn1a1a 80
Db 216 ATCCAGGAGTGTGACATCTATAGACCCCTTGGGCGCCCGCTGACATCCAGGCTGCC 275
Qy 81 GIn1aMetMetVal1ThrSerSerAla1eSerSer1eua1aCYa1le1SerVal1a 100
Db 276 CAGGCCATGATGGACATCCAGTCCATCTCTCCCTGGCTGATTAATCTGTGTG 335
Qy 101 GlyMetArgCYrThrVal1PheCYaGIn1uSerArg1a1yAspArgVal1aVal1a 120
Db 336 GGCATGAGATCAGACAGTCTTCTGCAGAGATCCGAGCAAGACAGAGTGGCGGTAGCA 395
Qy 121 GlyGlyVal1PhePhe1leuGlyGly1euleuGlyPhe1leProVal1Ala1TrpAsn1eu 140
Db 396 GGTGAGCTTTTTCATCTCTGAGGCTCTGGGATTCATCTCTGCTGCTGATCTT 455
Qy 141 HisGly1leuArgAspPheThySerPro1euVal1ProAspSerMet1yPheGlu1le 160
Db 456 CATGGATCTTACGGAGCTTCTACTCACCAGCTGTGCTGACAGCATAAATTGAGATT 515
Qy 161 GlyGluAla1eUry1eUgly1le1eSerSer1euPheSer1eua1e1aGly1le1le 180
Db 516 GGAGAGGCTTTTACTTGGCATTATTCTTCCCTGCTCCTCGATAGCTGGAATATC 575
Qy 181 LeuCYrPheSerCYrSerSerGInArgAsnArgSerAnt1yTYrAspAlaTYrGIn1a 200
Db 576 CTGCTCTTTCTGCTCATCCAGAAATCGCTCCACTGATGAGCTTACCAGCC 635
Qy 201 GInPro1euAla1ThrArgSerSerProArgProGlyGInPro1euVal1ySerGlu 220
Db 636 CAACCTCTTGCACAGAGCTCTCCAGGCTGTCACTCCCAAGTCAAGAGTAG 695
Qy 221 PheAsnSer1ySer1eUthnGlyTYrVal 230
Db 696 TTCAATTCCTACAGCTGACAGGATGTG 725
RESULT 4
ID AAA37060 standard; cDNA; 1475 BP.
XX AAA37060;
AC
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1356 (UNQ705) cDNA sequence SEQ ID NO:133.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS Homo sapiens.
XX
PN WC200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 02-SEP-1998; 98US-0098936P.
PR 02-SEP-1998; 98US-0098959P.
PR 02-SEP-1998; 98US-0098960P.
PR 02-SEP-1998; 98US-0098964P.
PR 02-SEP-1998; 98US-0098974P.
PR 02-SEP-1998; 98US-0098975P.
PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
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PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 24-SEP-1998; 98US-0102070P.
PR 24-SEP-1998; 98US-0102076P.
PR 24-SEP-1998; 98US-0102307P.
PR 24-SEP-1998; 98US-0102310P.
PR 24-SEP-1998; 98US-0102311P.
PR 24-SEP-1998; 98US-0102484P.
PR 24-SEP-1998; 98US-0102487P.
PR 24-SEP-1998; 98US-0102570P.
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PR 24-SEP-1998; 98US-0102687P.
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PR 24-SEP-1998; 98US-0103258P.
PR 24-SEP-1998; 98US-0103449P.
PR 24-SEP-1998; 98US-0103414P.
PR 24-SEP-1998; 98US-0103315P.
PR 24-SEP-1998; 98US-0103328P.
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PR 24-SEP-1998; 98US-0103401P.
PR 24-SEP-1998; 98US-0103633P.
PR 24-SEP-1998; 98US-0103678P.
PR 24-SEP-1998; 98US-0103679P.
PR 24-SEP-1998; 98US-0103711P.
PR 24-SEP-1998; 98US-0104257P.
PR 24-SEP-1998; 98US-0104987P.
PR 24-SEP-1998; 98US-0105000P.
PR 24-SEP-1998; 98US-0105002P.
PR 24-SEP-1998; 98US-0105104P.
PR 24-SEP-1998; 98US-0105169P.
PR 24-SEP-1998; 98US-0105266P.
PR 24-SEP-1998; 98US-0105633P.
PR 24-SEP-1998; 98US-0105694P.
PR 24-SEP-1998; 98US-0105807P.
PR 24-SEP-1998; 98US-0105881P.

PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Baker KP, Boltschein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
 PI Pan J, Peoni NF, Roy MA, Smith V, Stewart RA, Tumas D, Watanabe CK,
 PI Williams PM, Wood WI;
 DR WPI; 2001-071395/08.
 XX
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 PS Claim 2; Fig 77; 787p; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used used to generate either for
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatch: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-787-677a-3 (1-230) x AAF54296 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
 Db 122 ATGGCTCTCTTGGGCTTCACTGTGGGCTACATCCCTAGGCTTCTGGGCTTTGGGCT 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACGTGGTGGCAGTGGCTCCCACTGGAAACAAAGTTCTTATGTGGTGGCAGCACT 241
 QY 41 ValThrAlaValAlaGlyPheSerIleGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
 Db 242 GTGACAGAGAGTTGGCTTCTCCAAAGGCTCTGGAGGAAATGGCCACACAGCAGCAGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 Db 302 ATCAACCCAGTGTGACATCTATAGCACCTTCTGGGCTCCCGCTGACATCAGGCTGCC 361
 QY 81 GlnAlaMetMetValIleThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 362 CAGGCAATGATGGTACATCCAGTCAATCTCTCCCTGGGCTGATTAATCTCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnIleSerArgAlaValAspArgValAlaValAla 120
 Db 422 GGCAATGATGACACAGCTTCTCTCCAGGAATCCAGGCAAGACAGAGTGGCGTACCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 482 GGTGAGCTTTTTCATCTTGGAGGCTCTGGGATTCATTCCTGTTGCTCGAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGluIle 160
 Db 542 CATGGAGTCTACGGGACTTCTACTCACCTGGTGGCTGACAGCATAAATTTGAGATT 601
 QY 161 GlyAlaIleLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

Db 602 GGAGAGCTCTTACTGAGCATTAATTTCTCCCTGTTCCTCGATAGCTGGAATCATC 661
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerSerValTyrIlePheAlaTyrGlnAla 200
 Db 662 CTCTGCTTTTCTCGCTCATATCCAGAAATCGCTCCAACTACAGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPheValIleSerGlu 220
 Db 722 CAACCTTTTGGCACAGAGACTCTCCAGGCTGTGTCACTCCCAAGTCAGAGTGAAG 781
 QY 221 PheAsnSerTyrSerIleThrGlyTyrVal 230
 Db 782 TTCATTCCTACAGCTGACAGGATATGTG 811
 RESULT 6
 AAS21489
 ID AAS21489 standard; cDNA; 1475 BP.
 XX
 AC AAS21489;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human cDNA sequence encoding for PRO1356 polypeptide.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIa; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WC0200140466-A2.
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US032678.
 XX
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker KP, Beresini M, DeForge L, Deenoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR MPI; 2001-408281/43.
 DR P-PSDB; AAU12417.
 XX
 PT Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 3, Fig 491; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotide encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SO Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
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 QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 DB 122 ATGGCCCTCTTGCGCTCCCACTTGAGGCTGACATCTTACGCGCTTTGGGCG 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
 DB 182 ACACGTGTTGCCATGCTGCTCCGAGCTGAAAAACAAGTTCTTATGTCGGTCCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlnCysAlaThrHisSerThrGly 60
 DB 242 GTGACACAGTGGCTTCTCCCAAGGCTCTGATGTAATGTGCACACACAGACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlnGlyLeuProAlaAspIleGlnAla 80
 DB 302 ATCAACCAAGTGTACATCTAAGCACCTTCTGGGCTGCGCGTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 DB 362 CAGGCCATGTATGGTACATCAAGTCAATCTCTCTGCGCTGCGATTAATCTGTGTG 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
 DB 422 GGCATAGATGACACAGCTCTTCTGCGAGGAATCCCGACCAAAACAGAGTGGGTAGCA 481
 QY 121 GlyIValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPheLeu 140
 DB 482 GGTGAGCTCTTTTCACTTCCTTGAGAGCTCTCGGATTCATCTCTGCTGGAACTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIysPheGlu 160
 DB 542 CATGGATCCTACGGACCTTCACTACCACTGCTGCTGACAGCATGAATTTGAGATT 601
 QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 DB 602 GAGAGGCTCTTACTCTGGCATTAATTTCTCTCTCTCTGATGAGTGAATCATT 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAspTyrTyrAspAlaTyrGlnAla 200
 DB 662 CTCTGCTTTTCTGCTCATCTCCAGAAATCGTCCAACTACTACATGCTTCCAGGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIysValIysSerGlu 220
 DB 722 CAACCTCTTGCCCAAGAGAGCTTCCAGGCTGTGTCACCTCCAAAGTCAGAGTGAAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCATTTCTTCCACAGCTGACAGGATATGTG 811
 RESULT 7
 AAS15360
 ID AAS15360 standard; cDNA; 1475 BP.
 AC AAS15360;
 XX
 DT 16-JUN-2002 (first entry)
 XX
 DE cDNA encoding human PRO1356 polypeptide.
 XX
 KW Human; PRO1356; clone DNA64886-1601; immune-related disorder;
 KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
 KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
 KW neoplasia; transplantation associated disease; gene therapy;
 KW immunosuppressive; anti-inflammatory; antidiabetic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..814
 FT /tag= a
 FT /product= "PRO1356 polypeptide"
 FT sig_peptide 122..193
 FT /tag= b
 FT mat_peptide 194..811
 FT /tag= c
 FT
 PN WO200166740-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001MO-US006666.
 XX
 XX 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191015P.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 01-DEC-2000; 2000MO-US032678.
 XX
 PA (GETH) GENENTECH INC.
 PI Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL,
 PI Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI: 2001-625876/72.
 DR P-PSDB; AAU09178.
 XX Nucleic acids encoding PRO polypeptides, useful for detecting and
 PT treating immune related diseases and disorders in mammals including
 PT autoimmune diseases, inflammatory diseases and asthma.
 XX
 PS Claim 2; Fig 1; 122pp; English.
 XX
 CC The present invention relates to the isolation of 9 novel human PRO
 CC polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.
 CC The novel PRO polypeptides include PRO1356, PRO1884, PRO3444,
 CC PRO3151, PRO3322, PRO9964, PRO10008 and PRO19598. The cDNA sequences
 CC encoding these PRO polypeptides have been designated as clones DN6486-
 CC 1601, DN64903-1553, DN64318-2520, DN67997, DN69273, DN62223-2567,
 CC DN696973, DN6101921 and DN614587 respectively. Compositions (e.g.
 CC vaccines) containing PRO polypeptides and methods of using these
 CC compositions are useful in the treatment and diagnosis of immune-related
 CC disorders. Such disorders include immune-mediated inflammatory disorders
 CC (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.
 CC diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),
 CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.
 CC rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),
 CC demyelinating diseases of the peripheral or central nervous system (e.g.
 CC Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact
 CC dermatitis), neoplasias and transplantation associated diseases. The
 CC polynucleotide sequences of the invention may be used in gene therapy.
 CC AAS15360-AAS15366 represent cDNA sequences encoding for the novel human
 CC PRO polypeptides of the invention
 XX
 SO Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 6,72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-787-677A-3 (1-230) x AAS15360 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 122 ATGGCTCTCTTGGCTTCACTGTGGCTACATCTTCAAGCTTCTGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrrpYsrThrSerSerTyrValAlaSerIle 40
 Db 182 ACACGTGGTGGCAGTCTGCTCCCGACGTGAACAAATTCTTATGTCGGGCCAGCATT 241
 QY 41 ValThrAlaValAlGlyPheSerIleGlyLeuTrrpMetGluCyAlaIleHisSerThrGly 60
 Db 242 GTGACAGCAGTGGCTTCTCCAGGCGCTTGGAGATGTGCCACACAGCAGCAGC 301
 QY 61 IleThrGlnCyAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaIle 80
 Db 302 ATCACCCTGCTGACATCTTATGACACCTTCTGGGCTGCCCGCTGACATCCAGGCTCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCyAlaIleSerValVal 100
 Db 362 CAGGCGATGATGGTGAATCCAGTCAATCTCTCCGCTGCTGATATCTCTGTG 421
 QY 101 GlyMetArgCyTrnValPheCyGlnGlnSerArgAlaValAspArgValAlaValAla 120
 Db 422 GGCATGAGATCACAGTCTTCTGCGCAGGAATCCCGACGAAAGACAGTGGCGGTACA 481
 QY 121 GlyGlyValAlaPhePheIleLeuGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
 Db 482 GGTGAGCTCTTTTCATCTTGGAGGCTTCTGGGATTCATCTTGTGCTGGAGATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGlnIle 160

Db 542 CATGGATCTTACGGGAGCTTCTACTACACACTGTGCTGCAGCATGAATTTGAGATT 601
 QY 161 GlyGlnAlaLeuTyrIleLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GGAGAGGCTCTTATCTTGGGCAATTTCTTCCCTGTCTCCGATGACTGGATATC 661
 QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTACATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
 Db 722 CAACCTTGTGCACACAGAGCTCTCCAAAGCTGTGTCACCTCCCAAGTCAGAGTACG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCATTTCTTACAGCTTCAGACGGGTATGTG 811
 RESULT 8
 ID AAF92097 standard; cDNA; 1475 BP.
 XX AAF92097,
 AC AAF92097,
 XX 15-MAY-2001 (first entry)
 DT
 XX Human PRO1356 cDNA.
 DE
 XX Human, PRO protein; mapping; ss.
 XX Homo sapiens.
 OS
 XX WO200116318-A2.
 PN
 XX 08-MAR-2001.
 PD
 XX 24-AUG-2000; 2000WO-US023328.
 PF
 XX 01-SEP-1999; 99WO-US020111.
 XX 15-SEP-1999; 99WO-US021090.
 XX 07-DEC-1999; 99US-0169495P.
 XX 09-DEC-1999; 99US-0170262P.
 XX 11-JAN-2000; 2000US-015481P.
 XX 18-FEB-2000; 2000WO-US004341.
 XX 18-FEB-2000; 2000WO-US004342.
 XX 22-FEB-2000; 2000WO-US004414.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 03-MAR-2000; 2000US-0187202P.
 XX 21-MAR-2000; 2000US-0191007P.
 XX 30-MAR-2000; 2000WO-US008439.
 XX 25-APR-2000; 2000US-0199397P.
 XX 22-MAY-2000; 2000WO-US014042.
 XX 05-JUN-2000; 2000US-0209832P.
 XX
 PA (GENTH) GENE-TECH INC.
 XX
 XX Eason DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX
 XX WPI: 2001-183260/18.
 DR P-PSDB; AAB87565.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 PS Claim 2; Fig 79; 278pp; English.
 XX
 CC The present sequence is the coding sequence for a human PRO polypeptide
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
 CC antagonists or anti-PRO antibodies are useful for preparation of a
 CC medicament useful in the treatment of a condition which is responsive to
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6,72e-212	Length:	1475
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-787-677A-3 (1-230) x AAF92097 (1-1475)

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QY      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB      122 ATGGCCCTCTTGGCTCCACCTTGAGGCTACATCCTAGGCTTCTGGGGCTTTGGGC 181
QY      21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
DB      182 ACACTGGTTGCCACGCTGCTCCAGCTGGAACCAAGTTCTTATGCGGTCCAGCATT 241
QY      41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrIleSerThrGly 60
DB      242 GTACACAGCAGTGGCTTCTCCAGGGCTCTGAGTGAATGTCCACACACAGCAGCAGGC 301
QY      61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProIleAspIleGlnAlaAla 80
DB      302 ATCAACCAGTGTGACATCTATAGCACCTCTTGAGGCTGCGCTGATCCAGGCTGCC 361
QY      81 GlnAlaMetMetValTrpSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB      362 CAGGCCATGATGGGATCATCAGTCAATCTCCCTGGGCTGCAATTATCTCTGTGTG 421
QY      101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleValAlaValAla 120
DB      422 GGCATGATGATGACACAGCTCTTCTGCGCAGAAATCCCGACCAAGACAGTGGCGGTAGCA 481
QY      121 GlyGlyValPhePheIleLeuGlyIleLeuGlyIlePheIleProValAlaTrpAsnLeu 140
DB      482 GGTGGAGCTCTTTCATCTTGAGGCTCTCTGGGATTCATCTGTGCTGGAATCTT 541
QY      141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
DB      542 CATGGGATCTTACGGGACTTCTACTACACTGTGCTGACAGCAGCAATTTGAGATT 601
QY      161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB      602 GGAGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTCCCGATGAGTGGAAATCATC 661
QY      181 LeuCysPheSerCysSerSerGlnArgAsnArgSerTrpTyrAspAlaTyrGlnAla 200
DB      662 CTCTGCTTTCCTGCTATCCAGAGAAATGCTCCCACTACATACATGCTTACCAAGCC 721
QY      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValIleValSerGlu 220
DB      722 CAACCTCTTCCCAACAGAGACTCTCCAGGCGCTGTCACTCCCAAGTCAAGAGTGTG 781
QY      221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB      782 TTCAATTCTTACAGCTGACAGGATATGTG 811
```

RESULT 9

ABST74417
ID ABST74417 standard; cDNA; 1475 BP.

XX ABST74417;

XX 10-DEC-2002 (first entry)

DE Human cDNA encoding secreted/transmembrane protein PRO1356.

XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;

KW antiarthritic; osteopathic; sports-related joint problem;

KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

PN US2002119130-A1.

XX 29-AUG-2002.

PF 06-DEC-2001; 2001US-00006867.

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XX      29-OCT-1997; 97US-0063435P.
XX      29-OCT-1997; 97US-0064215P.
PR      22-APR-1998; 98US-0082797P.
PR      29-APR-1998; 98US-0083495P.
PR      15-MAY-1998; 98US-0085579P.
PR      02-JUN-1998; 98US-0087759P.
PR      04-JUN-1998; 98US-0088021P.
PR      04-JUN-1998; 98US-0088029P.
PR      04-JUN-1998; 98US-0088030P.
PR      10-JUN-1998; 98US-0088734P.
PR      10-JUN-1998; 98US-0088740P.
PR      10-JUN-1998; 98US-0088811P.
PR      10-JUN-1998; 98US-0088824P.
PR      10-JUN-1998; 98US-0088825P.
PR      11-JUN-1998; 98US-0088863P.
PR      12-JUN-1998; 98US-0089105P.
PR      15-JUN-1998; 98US-0089514P.
PR      17-JUN-1998; 98US-0089653P.
PR      19-JUN-1998; 98US-0089952P.
PR      22-JUN-1998; 98US-0090246P.
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PR      25-JUN-1998; 98US-0090696P.
PR      26-JUN-1998; 98US-0090862P.
PR      02-JUL-1998; 98US-0091628P.
PR      10-AUG-1998; 98US-0096012P.
PR      17-AUG-1998; 98US-0096757P.
PR      18-AUG-1998; 98US-0096949P.
PR      18-AUG-1998; 98US-0096959P.
PR      26-AUG-1998; 98US-0097954P.
PR      26-AUG-1998; 98US-0097971P.
PR      26-AUG-1998; 98US-0097979P.
PR      01-SEP-1998; 98US-0098749P.
PR      10-SEP-1998; 98US-0099741P.
PR      10-SEP-1998; 98US-0099763P.
PR      10-SEP-1998; 98US-0099792P.
PR      10-SEP-1998; 98US-0099812P.
PR      10-SEP-1998; 98US-0099815P.
PR      16-SEP-1998; 98US-0100627P.
PR      16-SEP-1998; 98US-0100652P.
PR      16-SEP-1998; 98US-0100662P.
PR      16-SEP-1998; 98US-01019330.
PR      17-SEP-1998; 98US-0100683P.
PR      17-SEP-1998; 98US-0100684P.
PR      17-SEP-1998; 98US-0100930P.
PR      17-SEP-1998; 98US-0101279P.
PR      22-SEP-1998; 98US-0101475P.
PR      23-SEP-1998; 98US-0101738P.
PR      24-SEP-1998; 98US-0101743P.
PR      24-SEP-1998; 98US-0101916P.
PR      24-SEP-1998; 98US-0102570P.
PR      30-SEP-1998; 98US-0103449P.
PR      06-OCT-1998; 98US-0103499P.
PR      08-MAR-1999; 99MO-US005028.
PR      14-MAY-1999; 99MO-US010733.
PR      02-JUN-1999; 99MO-US012252.
PR      01-SEP-1999; 99MO-US020111.
PR      15-SEP-1999; 99MO-US021090.
PR      15-SEP-1999; 99MO-US021194.
PR      22-DEC-1999; 99MO-US030720.
PR      18-FEB-2000; 2000MO-US004341.
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PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023378.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 01-DEC-2000; 2000MO-US032378.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001MO-US006666.
 PR 01-MAR-2001; 2001MO-US006666.
 PR 30-MAY-2001; 2001MO-US017443.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 PA (GERTH) GENENTECH INC.
 PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WT;
 XX WPI; 2002-731348/79.
 DR P-PSDB; ABG95890.
 XX
 PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 XX
 PS Claim 2; Fig 79; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the

CC invention
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-787-677a-3 (1-230) x ABS74417 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnIleuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 DB 122 ATGGCTCTCTGGCTCCCACTTGAGGCTTACCTTACCTTCTGGGCTTTGGGC 181
 QY 21 ThrIleuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
 DB 182 ACACGTGGTGGCAATGCTGCTCCCACTGGAAACAAAGTTCTTATGTCGGTCCAGCATT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
 DB 242 GTGACAGCAGTGGCTCTCCAAAGGCTCTGATGTAATGTGCACACACAGCAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 302 ATCCACCAAGTGTGACATCTATAGACCTCTGGGCTTGGCCCTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 362 CAGGCCATGATGATGATCATCATCAGATCATCTCCCTGGGCTCATATCTGTGCTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaAlaValAlaAla 120
 DB 422 GGCACTGAGATGACAGCTCTCTGCAAGATCCAGACCAAGACAGAGTGGCCGTGACA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrAsnLeu 140
 DB 482 GGTGAGCTTTTCACTTCACTTGGAGGCTCTGGAAATTCATTCTTGTGCTGGAACTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 542 CATGGATTCCTAGCGGACTTCACTACCACTGCTGCTGACACATGAATTTGAGATT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 602 GGAAGAGCTCTTTACTTGGCATTAATTCCTCTGTTCCCTGATGACGTGATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 DB 662 CTGCTCTTCTCTCTCAATCCACAGAAATGCTCCCACTACATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 DB 722 CAACCTCTTGGCACAAGAGCTCTCCAAAGCTGTGTCACTCCCAAGTAAAGAGGAG 781
 QY 221 PheIleuSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCAATTCCTACACCTGACAGGAGTATGTG 811
 RESULT 10
 ABL88167
 ID ABL88167 standard; cDNA; 1475 BP.
 XX
 AC ABL88167;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO1356 cDNA sequence SEQ ID NO:191.
 XX
 KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;

KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiotensin disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping; gene; ss.
 XX Homo sapiens.
 OS WO20020690-A2.
 PN 03-JAN-2002.
 XX 20-JUN-2001; 2001WO-US019692.
 PF 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001US-00066666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AI, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR P-PSDB; ABB84912.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 2; Fig 191; 565pp; English.
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Score: 6,72e-212 Length: 1475
 Percent Similarity: 230.00 Matches: 230
 Best Local Similarity: 100.00* Conservative: 0
 Query Match: 100.00* Mismatches: 0
 DB: 6 Gaps: 0
 US-09-787-677a-3 (1-230) x ABL88167 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlnGlyLeuGly 20
 Db 122 ATGGCCCTCTTGGCCCTCAACTTGGGCTACATCTTAAGCCCTTGGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrThrSerTyrValGlyAlaSerIle 40
 Db 182 ACACTGGTTCACATGCTGCTCCAGCTGAGAAACAAGTTCCTAATGCGTGCAGCATT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThGly 60
 Db 242 GTGACGACATGAGCTTCTCCAGGGCTCTGAGTGAATGTCACACACAGCAGCGCC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 Db 302 ATCACCCAGTGTGACATCTATAGACCCCTTGGGCTGCCCGTGCATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 362 CAGGCCATGATGTGATCATCATCAGTGCATCTCCCTGCGCTGCATTATCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaVal 120
 Db 422 GGCATGATGATCCAGATCTTCTGCGAGATCCGAGCCAAAGACAGTGGCGATGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaIlePasnLeu 140
 Db 482 GGTGAGTCTTTTTCATCTTGGAGGCTCTCGGATTCATTCCTGTGCTGGAACTT 541
 QY 141 HisGlyIleLeuAlaArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 160
 Db 542 CATGGATCTTACGGGACTTCTTACTCCACCTGGTGTCTACAGCATGAATTTGAGATT 601
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GGAAGGCTCTTACTTGGCATTTATTTCTCCCTGTTCTCCGTGATGCTGGAATATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACATGCTCCCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 Db 722 CAACCTCTTCCCAAGAGACTCTCCAAAGGCTGTGATCACTCCCAAGTCAAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGATATGTG 811
 RESULT 11
 ID ABLK1089 standard; cDNA; 1475 BP.
 XX

AC ABK11089;
XX 05-JUN-2002 (first entry)
XX cDNA encoding tumour-associated antigenic target protein, TAT134.
XX TAT134: Tumour-associated Antigenic Target; tumour; breast cancer;
XX colorectal cancer; lung cancer; ovarian cancer;
XX central nervous system cancer; liver cancer; bladder cancer; melanoma;
XX pancreatic cancer; leukaemia; gene therapy; gene; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 122..814
XX /tag= a
XX /product= "TAT134"
XX /note= "Tumour-associated antigenic target"
XX
XX WO200216429-A2.
XX
XX 28-FEB-2002.
XX
XX 22-JUN-2001; 2001WO-US020118.
XX
XX 24-AUG-2000; 2000WO-US023328.
XX 26-SEP-2000; 2000US-0235451P.
XX 01-DEC-2000; 2000WO-US032678.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX
XX (GETH) GENENTECH INC.
XX
XX Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,
XX Wood WI, Wu TD, Zhang Z;
XX WPI: 2002-280917/32.
XX P-PSDB; MAU76534.
XX
XX Novel isolated tumor-associated antigenic target polypeptides which are
XX useful as targets for cancer therapy and diagnosis in mammals.
XX
XX Claim 1; Fig.1; 121pp; English.
XX
XX The invention relates to an isolated tumour-associated antigenic target
XX polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the
XX polynucleotides (II) encoding them. (II) is useful for diagnosing the
XX presence of a tumour in a mammal, where the level of expression of (II)
XX is indicative on the presence of tumour in the mammal from which the test
XX sample was obtained. Antibody to (I) is useful for killing a cancer cell,
XX (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,
XX an ovarian cancer cell, a central nervous system (CNS) cancer cell, a
XX liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a
XX melanoma cell or a leukaemia cell) that expresses (I). Oligonucleotides
XX hybridising to (II) are useful as diagnostic probes, antisense
XX oligonucleotide probes or for encoding fragments of full length TAT
XX polypeptide. (II) is also useful in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA probes, for constructing
XX hybridisation probes for mapping the gene encoding TAT and for genetic
XX analysis of individuals with genetic disorders. (II) is also useful for
XX generating either transgenic animals or knockout animals, and in gene
XX therapy. The TAT polypeptides and nucleic acids may also be used for
XX tissue typing and the TAT polypeptides are useful for screening compounds
XX that mimic the TAT polypeptide (agonist) or prevent the effect of TAT
XX polypeptide (antagonist). The antibody is useful for staging TAT
XX polypeptide-expressing cancers, purifying or immunoprecipitating TAT
XX polypeptide from cells, for detection and quantitation of TAT polypeptide
XX in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
XX Western blot. The antibodies are also useful for treating a TAT-
XX expressing cancer or alleviating one or more symptoms of cancer in a
XX mammal. The present sequence represents the coding sequence of TAT134
XX
XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,72e-212 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-787-677a-3 (1-230) x ABK11089 (1-1475)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlnGlyLeuGly 20
DB 122 ATGGCTCTCTTGGCCCTCCAACTTGCGCTACATCTAGGCCCTTGGGGCTTTGGCC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTTPlyThrSerSerTyrValGlyAlaSerIle 40
DB 182 ACATGGGTGGCAATGCTGCTCCCAAGCTGGAACAAAGTTCTTATGCGGTGCCAGCAT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
DB 242 GTGACAGCAGTGGCTCTCCAAAGGCTCTGGATGAAATGTCACACACAGCAGCAGC 301
QY 61 IleThrGlnCysApeIleTyrSerThrLeuLeuGlyLeuProAlaApeIleGlnAla 80
DB 302 ATCACCAGGTGATCATCTATAGCACCCCTTGGGCTGCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGGGAGATCCAGATCCAGATCTCCCTGGCTGGCATTTATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
DB 422 GGCATGAGATGACAGCTCTTCTCCAGAAATCCGAGCAACAAAGACAGTGGCGTGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlnGlyPheIleProValAlaTTPAsnLeu 140
DB 482 GGTGAGCTTTTTCATCTTGAGGCTCTGGGATTTCAATCTGTTGCTGGAAATCTT 541
QY 141 HisGlyIleLeuAlaGAspPheTyrSerProLeuValProAspSerMetClyPheGluIle 160
DB 542 CATGGATCTCCACGGGACTTCTACTCACCACTGTGTGCTTCAACAGCATGAATTTGAAAT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
DB 602 GGAAGGCTCTTTCATCTTGAGGATTAATTTCTCTGTTCTCGATAGCTGMAATATC 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAntTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCTGCTTTTCTGCTCATCCAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValysSerGlu 220
DB 722 CAACTCTTGGCAAGAGGCTCTCCAAAGGCTGTGTAACCTCCCAAGTCAAGAGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAATTCCTACAGCTTACAGGATATGTG 811
RESULT 12
ABL95656 standard; cDNA; 1475 BP.
ID ABL95656
AC ABL95656;
XX 19-JUN-2002 (first entry)
XX
XX Human angiogenesis related cDNA PRO1356 SEQ ID NO: 191.
XX
XX Human; angiogenesis; PEO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX cardiac; cytosolic; antiangiogenic; hypotensive; vulnary;
XX antiarteriosclerotic; gene; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US021735.
 XX
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222685P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030952.
 PR 10-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00766498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 XX
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERR/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLMAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANT/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI: 2002-171999/22.
 DR P-PSDB: ABB95518.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

PS Claim 1; Fig 191; 567bp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention
 XX
 SO Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.72e-212 Length: 1475
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-787-677A-3 (1-230) x ABB95556 (1-1475)
 QY 1 MetAlaserleuGlyleuGlnleuValAlGlyTyrIleleuGlyleuGlyleuGlyleuGly 20
 Db 122 ATGGCTCTTGGCTTCCCACTTGTGGCTCACTCACTCACTCACTTGTGGCTTGTGGCT 181
 QY 21 ThrleuValAlMetleuLeuProSerTyrPheThrSerSerTyrValAlGlyAlaserile 40
 Db 182 ACACTGGTTCACATGCTGCTCCCACTGAGTGAACAAAGTTCCTTATGCGGTGCAGCATT 241
 QY 41 ValThrAlaValAlGlyPheSerIleGlyleuTyrMetGluCysAlaThrHisSerThrGly 60
 Db 242 GTGACACAGCACTTGGCTTCCCAAGGCTCTGATGGAATGTCACACACACACACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrleuGlyleuProAlaAspIleGlnAlaAla 80
 Db 302 ATCAACCAAGTGTACATCTTACACCTTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerValAl 100
 Db 362 CAGGCCATGATGGATGACATCACTGATGATCTCTCCCTGCTGCTGCTGCTGCTGCTGCT 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerAlaAlaValAspArgValAlaValAla 120
 Db 422 GGCATGATGATGACAGCTTCTGCTGCAAGATCCCGAGCCAAAGACAGAGTGGGATGCA 481
 QY 121 GlyIleValPhePheIleleuGlyIleleuGlyPheIleProValAlaTyrPantleu 140
 Db 482 GGTGAGATCTTTCATCTTGAAGGCTCTGGAATTCATCTCTGCTGCTGGAATCTT 541
 QY 141 HisGlyIleleuArgAspPheTyrSerProleuValProAspSerMetLysPheGluIle 160
 Db 542 CATGGATCTTACGGAGCTTCTACTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
 QY 161 GlyGlnAlaLeuTyrleuGlyIleIleSerSerleuPheSerleuIleAlaGlyIleIle 180
 Db 602 GGAGAGGCTCTTACTTGGGCTGATTAATTTCTCCCTGTTCTCCCTGATGATGATATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAspTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCGCTTTCCTGCTCATCTCCAGAGAAATCGCTCCCACTCACTCACTCACTCACTCACT 721
 QY 201 GlnProleuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 Db 722 CAACCTCTTCCCAAGAGCTCTCCCAAGGCTGATCACTCACTCACTCACTCACTCACTCACT 781
 QY 221 PheAsnSerTyrSerleuThrGlyTyrVal 230
 Db 782 TTCATTTCTTACAGCTGACAGGATATGTG 811
 RESULT 13
 ACA91203

ID ACA91203 standard; cDNA; 1475 BP.
XX
AC ACA91203;
XX
DT 11-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1356 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antibody therapy;
KM pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003018173-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063515.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GERTH) GENENTECH INC.
XX
PI Baton DL, Filvaroff E, Gerltzen ME, Goddard A, Godowski PU;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-401702/38.
DR P-PSDB; AB090915.
XX
PT New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.
XX
PS Disclosure; Fig 79; 345BP; English.
XX
CC The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.72e-212 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-09-787-677a-3 (1-230) x ACA91203 (1-1475)
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QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheTyrSerSerTyrValGlyAlaSerIle 40
DB 182 ACACGTGTTGCATCTGCTCCCGACGTGAAGAAACAAAGTTCTTATGTGCGTGCACGATT 241
QY 41 ValThrAlaValAlaGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
DB 242 GTGACAGCAGTGTGCTTCCAAAGGCTCTGGAATGATGCGCACACAGCAGCAGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80

DB 302 ATCACCAGTGTGACATCTATAGACACCTCTGGGCTGCCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValIleThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 362 CAGGCCATGATGGATGACATCAGATCATCTCTCCCTGGCTGACATTAATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
DB 422 GGCATGATGATGACAGCTCTTCTGCGAGGATCCGAGCAAAAGACAGAGGGGTGCA 481
QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPheLeu 140
DB 482 GGTGAGCTTTTTCATCTTGAGGCTCTGAGGATTCATTCCTGCTGCAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
DB 542 CATGGATCCTTACGGGCTTCTACTCACCTGGTGTGACAGCATGAATTTGACATT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
DB 602 GGAGAGCTCTTTACTTGGGCTATTCTTCCCTGTTCTCTGATAGCTGAAATCATC 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAntTyrAspAlaTyrGlnAla 200
DB 662 CTCTGCTTTCTCTGCTCATCCAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlySValIleSerGlu 220
DB 722 CAACCTTTGCCACAAAGACCTCTCCAAAGCTGTGTCAACCTCCCAAGATCAAGATGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAATTCCTACAGCTTCAAGGATATGTG 811
RESULT 14
ACD81580
ID ACD81580 standard; cDNA; 1475 BP.
XX
AC ACD81580;
XX
DT 18-SEP-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1356.
DE Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
KM cytosolic.
XX
OS Homo sapiens.
XX
PN US2003009013-A1.
XX
PD 09-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063519.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.

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PR    02-JUN-2000; 200OWO-US015264.
PR    22-AUG-2000; 2000US-00644848.
PR    24-AUG-2000; 200OWO-US023328.
PR    18-SEP-2000; 2000US-00664610.
PR    18-SEP-2000; 2000US-00665350.
PR    08-NOV-2000; 2000US-00709238.
PR    10-NOV-2000; 200OWO-US030873.
PR    01-DEC-2000; 200OWO-US032678.
PR    20-DEC-2000; 2000US-00747259.
PR    20-DEC-2000; 200OWO-US034956.
PR    28-FEB-2001; 200LWO-US006520.
PR    22-MAR-2001; 200LWO-US016744.
PR    10-MAY-2001; 200LWS-00854208.
PR    10-MAY-2001; 200LWS-00854280.
PR    30-MAY-2001; 200LWS-00870574.
PR    01-JUN-2001; 200LWO-US017800.
PR    05-JUN-2001; 200LWS-00874503.
PR    29-JUN-2001; 200LWS-00869599.
PR    18-JUL-2001; 200LWS-00908827.
PR    06-DEC-2001; 200LWS-00005867.

XX
XX
PA    (GETH ) GENENTECH INC.
PI    Eamon DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI    Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;
XX
DR    WPI: 2003-447384/42.
XX    P-PsDB; ABO33974.
XX
PT    New isolated antibody specifically binding a PRO polypeptide, useful for
PT    expression or activity of the PRO polypeptide, such as tumor conditions
XX
XX
XX    Disclosure; Fig 79; 223pd; English.
XX
CC    The invention relates to an antibody that binds to a secreted or
CC    transmembrane protein designated PRO1446 appearing as ABO33941. The
CC    protein is one of 84 PRO polypeptides which (along with their encoding
CC    nucleic acids) are disclosed in the specification. The methods and
CC    compositions of the present invention are useful for the preparation of a
CC    medicament for the treatment of disorders associated with the aberrant
CC    expression or activity of the PRO polypeptide, such as tumour conditions
CC    and cancer. They can also be used to generate transgenic or knockout
CC    animals useful in the development and screening of therapeutically useful
CC    reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC    molecular weight markers for protein electrophoresis, chromosome
CC    identification and tissue typing. The antibodies may be used in various
CC    diagnostic, competitive binding and/or immunoprecipitation assays. The
XX    present sequence encodes a PRO polypeptide
XX
SQ    Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Align. No.:      6 72e-212          Length:      1475
Score:           230.00             Matches:     230
Percent Similarity: 100.00%         Conservative: 0
Best Local Similarity: 100.00%       Mismatches:  0
Query Match:     100.00%            Indels:      0
                                DB:           Gaps:      0

US-09-787-677A-3 (1-230) x ACD81580 (1-1475)

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Db    122 ANGGGCTCtTGgCcTCcCAACttGTtgGCGGTAcATcctTAGcCTTtcGGGC 181
QY    21 ThrIeuValAlMeMetIeuLeuPProSerTrPyLeThrSeSerTyRyValAGlyAlaSerIle 40
Db    182 ACACtGGtTGCAtGTgcTccCACcCTGAACAAGTTCTTAgtCGGTGCCAgCATT 241
QY    41 ValThrAlaValAGlyPhseSerLySGlyleuTrpMetGIuCyValatRhIssetRhGly 60

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Db	242	GNAGACAGACGCTGGCCTTCC	AAGGGCCCTCGGATGGATGTG	CCACACAGACAGGC	301
Oy	61	11ethrglnCysasp11e	tyrSerThrLeuLeuGlyLeuProAlaasp11e	glnAla1a	80
Db	302	ATCACCACAGTGTGACATCTAT	AGCACCCCTTCGGGGCTGCC	CCGCTGACATCCAGGGCTGC	361
Oy	81	glnAlaMetValThrSerSerAla	1eSerSerLeuAlaCys11e	1eSerVal1a	100
Db	362	CAGGGCCATGATGATGACATCC	AGTCGATCTCTCCCTGGCCTG	CACTATCTCTGTGGTG	421
Oy	101	GlyMetArgCysThrValPhe	CysGlnGlnSerArgAlaLys	aspArgValAla1a1a	120
Db	422	GGCATGAGATGACAGCTCTT	CGCAGAGATCCCGAGCCAA	AGACAGAGTGGCGGTAGCA	481
Oy	121	GlyGlyValPhePhe11e	LeuGlyGlyLeuLeuGlyPhe11e	ProValAla1a	140
Db	482	GGTGAAGTCTTTTTCATCTT	GGAGGCCCTCGGATTCATTC	CTGTGCTGGAAATCTT	541
Oy	141	H1aGly11eLeuArgAspPhe	TyrSerProLeuValProAsp	SerMetLysPheGlu11e	160
Db	542	CATGGATCTTACGGGACTT	CTACTACACACGTGGTCC	TGACAGCATGAAATTTGAGATT	601
Oy	161	GlyGlnAlaLeuTyrLeuGly	11e11eSerSerLeuPheSer	Leu11eAlaGly11e11e	180
Db	602	GGAGAGGCGCTTACTCTTG	GGCATATTTCTTCCCTTCT	CCCTGATAGCTGAAATCATC	661
Oy	181	LeuCysPheSerCysSerSer	GlnArgAsnArgSerAsnTyr	TyrAspAla1aTyrGlnAla	200
Db	662	CTCTCTTTTCTGCTCATCC	CAGAGAAATCGCTCAACT	ACTACGATGCTTACCAAGCC	721
Oy	201	GlnProLeuAla1aThrArg	SerProArgProGlyGlnPro	ProLysValLysSerGlu	220
Db	722	CAACCTCTTGCCACAGAG	AGCTCTCCAGGCGCTGTG	CAACTCCCAAAAGTCAGAGT	781
Oy	221	PheAsnSerTyrSerLeuThr	GlyTyrVal	230	
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RESULT 15					
ACA60402					
ID	ACA60402	strand; cDNA; 1475 BP.			
XX	ACA60402;				
AC					
XX					
DT	11-JUN-2003	(first entry)			
XX					
DE		Novel human secreted and transmembrane protein PRO1356 cDNA.			
XX					
KM		Human; secreted and transmembrane polypeptide; gene;			
KW		ss. chromosome mappng; gene mappng; transgenic animal; knockout animal;			
KM		therapeutic agent screening; chromosome identification; tissue typing;			
XX		gene therapy.			
XX					
OS	Homo sapiens.				
XX					
FN	US2003018183-A1.				
XX					
PD	23-JAN-2003.				
XX					
PF	01-MAY-2002; 2002US	-00063512.			
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PR	06-DEC-2001; 2001US	-00006867.			
XX					
PA	(GETH) GENENTECH INC.				
XX					
PI	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;				
XX	Grimaldi JC, Gurney AL, Watanabe CK, Wood WT;				
XX	WPI; 2003-330984/31.				
DR	P-PSDB; ABU71991.				
XX					
PT	New secreted and transmembrane PRO polypeptides and nucleic acid molecules encoding the polypeptides, useful in gene therapy or preparing				

PT a medicament for treating a condition that is responsive to the PRO
PT polypeptide or antibody.

PS Disclosure; Fig 79; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.72e-212	Length:	1475
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-09-787-677a-3 (1-230) x ACA60402 (1-1475)

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Db 122 ATGGCTCTCTTGGCTCCCACTGTGGGTACATCTAGGCTTCTGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
Db 182 ACAGTGTGGCTGCTGCTCCCAAGGAAACAGTCTTGTGTCGACGACATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTGACAGCATTTGGCTTCCAGAGGCTCTGGATGATGTGCCACACAGCAGAGCC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCAGTGTGACATCTATAGCACCTTCTGGGCTGCCGCTGACATCTCTGTGTG 421
QY 101 GlyMetArgCysTrpValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
Db 422 GGCATGAGATGACAGTCTTCTGCCAGGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTrpAsnLeu 140
Db 482 GGTGAGATCTTTTTCATCTCTGAGGCTCTCTGGGATTCATTCTCTGCTGGATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGlnIle 160
Db 542 CATGGATCTTACGGGATCTTACTACACCTGCTGCTGACAGCATGATAAATTGAGATT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGAGCTCTTACTTGGCATTTATTTCTTCCCTGTTCTCCCTGATAGCTGGATCATC 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCGCTTTTCTGTCTCATCCAGAGAAATGCTCTCACTACTAGATGCTTACCAAGCC 721
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QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db 722 CAACCTTTGCGACAGAGAGCTCTCCAGGCTTGGTCAACTCTCCAAAGTCAGAGATGAG 781
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QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
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Search completed: December 20, 2004, 18:16:05
Job time : 501 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 18:07:46 ; Search time 95 Seconds
(without alignments)
1720.857 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230
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Searched: 824507 seqs, 355394441 residues

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Total number of hits satisfying chosen parameters: 1643622

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	230	100.0	1475	4	US-10-140-002-491
3	127	55.2	1524	4	US-09-663-600A-45
4	5	3.9	627	4	US-09-252-991A-6070
5	4	3.9	630	4	US-09-252-991A-6398
6	3	3.9	873	4	US-09-252-991A-6226
7	8	3.5	410	3	US-09-114-146-1
8	8	3.5	410	5	PCT-US96-08623-1
9	8	3.5	417	4	US-09-252-991A-257
10	8	3.5	709	2	US-08-844-120-2
11	8	3.5	709	2	US-09-022-940-2
12	8	3.5	709	3	US-09-216-386-2

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14	8	3.5	714	4	US-09-252-991A-1683	Sequence 1683, Ap
15	8	3.5	753	4	US-09-270-767-1386	Sequence 1386, Ap
16	8	3.5	753	4	US-09-270-767-16668	Sequence 16668, A
17	8	3.5	846	4	US-09-270-767-12047	Sequence 12047, A
18	8	3.5	930	4	US-09-252-991A-1404	Sequence 1404, Ap
19	8	3.5	1002	4	US-09-252-991A-11872	Sequence 11872, A
20	8	3.5	1008	4	US-09-248-796A-3558	Sequence 3558, Ap
21	8	3.5	1284	3	US-09-134-001C-212	Sequence 212, App
22	8	3.5	1386	4	US-10-182-263-9	Sequence 9, Appl1
23	8	3.5	1386	4	US-10-182-263-10	Sequence 10, Appl1
24	8	3.5	1386	4	US-10-182-263-11	Sequence 11, Appl1
25	8	3.5	1386	4	US-10-182-263-12	Sequence 12, Appl1
26	8	3.5	1389	4	US-09-252-991A-4243	Sequence 4243, Ap
27	8	3.5	1437	4	US-09-252-991A-1434	Sequence 1434, Ap
28	8	3.5	1464	4	US-09-252-991A-11508	Sequence 11508, A
29	8	3.5	1473	4	US-09-252-991A-1584	Sequence 1584, Ap
30	8	3.5	1611	4	US-09-534-743-1	Sequence 1, Appl1
31	8	3.5	1611	4	US-09-534-743-3	Sequence 3, Appl1
32	8	3.5	1629	4	US-09-252-991A-11733	Sequence 11733, A
33	8	3.5	1941	4	US-09-252-991A-248	Sequence 248, App
34	8	3.5	1995	4	US-09-252-991A-14545	Sequence 14545, A
35	8	3.5	2022	4	US-09-252-991A-1152	Sequence 1152, Ap
36	8	3.5	2470	3	US-09-091-725-18	Sequence 18, Appl1
37	8	3.5	2546	3	US-09-091-725-12	Sequence 12, Appl1
38	8	3.5	2588	4	US-09-252-991A-4323	Sequence 4323, Ap
39	8	3.5	2859	4	US-09-853-180B-1	Sequence 1, Appl1
40	8	3.5	2874	4	US-09-252-991A-4533	Sequence 4533, Ap
41	8	3.5	3084	4	US-09-252-991A-1315	Sequence 1315, Ap
42	8	3.5	3090	4	US-09-016-434-1397	Sequence 1397, Ap
43	8	3.5	3108	4	US-09-614-221A-194	Sequence 194, App
44	8	3.5	3396	4	US-09-252-991A-14676	Sequence 14676, A
45	8	3.5	3444	4	US-09-252-991A-15078	Sequence 15078, A

ALIGNMENTS

RESULT 1
US-09-663-600A-139
; Sequence 139, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouguerelet, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent .pm
; SEQ ID NO 139
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 36..107
; OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 5.6999980926514
 OTHER INFORMATION: seq ILGLGLGLTVA/ML
 NAME/KEY: polya_signal
 LOCATION: 1302..1307
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 LOCATION: 1389..1400
 US-09-663-600A-139

Alignment Scores:

Pred. No.:	6.97e-214	Length:	1400
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-09-787-677A-3 (1-230) x US-09-663-600A-139 (1-1400)

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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly
Db 36 ATGGCCCTCTTGGCCCTCACTTGTGGCTACATCTTAAGCCCTTCTGGGGCTTTGGGC
Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle
Db 96 ACACGTGTCCTGCTGCTGCCACGTGGAACAAAGTTCTTATGTCGGTGCACGATC
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThyGly
Db 156 GTACACGACATGGCTTCTCCAAAGGCTCTGATGGAATGTGCACACACAGCAGGC
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla
Db 216 ATCAACCAAGTGTACATCTATAGCACCCCTTCTGGCCCTGCGGTGACATCCAGGCTGCC
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal
Db 276 CAGGCGCATGATGGACATCAGATGACATCTCCCTGGCTGCTCATATCTCTGTGTG
Qy 101 GlnMetArgCysThrValPheCysGlnGluSerArgAlaValAspArgValAlaValAla
Db 336 GGCATGAGATGACAGCTTCTGTCAGAGAAATCCGAGCCAAAGACAGATGGCGGTAGCA
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaATrPAsnLeu
Db 396 GGTGGAGCTCTTTTCATCTTTGAGGCTCTCTGGATTCATCTCTGTGCTGGAATCTT
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle
Db 456 CATGGGATCTTACGGGACTTCTACTCACCACTGGTGCCTGACACATGAATTTGAAGATT
Qy 161 GlyGlnAlaLeuTyrIleGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle
Db 516 GGAAGAGCTCTTAACTTGGGATTAATTTCTCTCTCTCCCTGATGACGAGATATC
Qy 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla
Db 576 CTCTGCTTTCTCTCTCATCTCCAGAGAAATGCTCCAACTACTACATGCTCTACCAAGCC
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValLysSerGlu
Db 636 CAACCTCTTCCACAAAGAGCTCTCCAAAGCTGTGTCAACTCCCAAGTCAAGAGTAGAG
Qy 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 696 TTCATATCTTACACGCTGACAGGGATATGTG 725

```

RESULT 2
 US-10-140-002-491
 Sequence 491 Application US/10140002
 Patent No. 6725730
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen

```

APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Mei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowsky, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 491
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-002-491

```

Alignment Scores:

Pred. No.:	7.33e-214	Length:	1475
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	4	Gaps:	0

US-09-787-677A-3 (1-230) x US-10-140-002-491 (1-1475)

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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly
Db 122 ATGGCCCTCTTGGCCCTCACTTGTGGCTACATCTTAAGCCCTTCTGGGGCTTTGGGC
Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle
Db 182 ACACGTGTCCTGCTGCTGCCACGTGGAACAAAGTTCTTATGTCGGTGCACGATC
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThyGly
Db 242 GTACACGACATGGCTTCTCCAAAGGCTCTGATGGAATGTGCACACACAGCAGGC
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla
Db 302 ATCAACCAAGTGTACATCTATAGCACCCCTTCTGGCCCTGCGGTGACATCCAGGCTGCC
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal
Db 362 CAGGCGCATGATGGATCATATAGCACCCCTTCTGGCTGCGGTGACATCTCTGTGTG
Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaValAspArgValAlaValAla
Db 422 GGCATGAGATGACACAGCTTCTCTCCAGGAATCCGAGCCAAAGACAGAGTGGGTAGCA
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaATrPAsnLeu
Db 482 GGTGGAGCTCTTTTCATCTTTGAGGCTCTCTGGATTAATCTCTGTGCTGGAATCTT
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle
Db 542 CATGGATCTTACGGGACTTCTACTCACCACTGGTGTGACAGCATGAATTTGAGATT
Qy 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle
Db 602 GGAAGAGCTCTTAACTTGGGATTAATTTCTCTCTCTCTGATGATGATATCATC

```

QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCCTGCTTTTCCGCTCATCTCCAGAGAAATCGCTCCAATCACTACGATGCTTCCAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 722 CAACCTCTTGCCACAGAGACCTCTCCAGGCGCTGGTCAACCTCCCAAGTCAGAGAGTAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATTTCCACAGCGCTGACAGGATATGTG 811
RESULT 3
US-09-663-600A-45
Sequence 45, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclercq, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 45
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig peptide
LOCATION: 160..231
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6999980926514
NAME/KEY: polyA_signal
LOCATION: 1510..1515
NAME/KEY: polyA_site
LOCATION: 1506..1519
NAME/KEY: misc_feature
LOCATION: 1048..1504
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA552647
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 597..846
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA345449
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 39..53
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA345449
NAME/KEY: misc_feature
LOCATION: 113..149
OTHER INFORMATION: homology

OTHER INFORMATION: id: AA345449
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 98..400
OTHER INFORMATION: homology
OTHER INFORMATION: id: T86266
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 1210..1489
OTHER INFORMATION: homology
OTHER INFORMATION: id: T86158
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 954..983
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA116709
OTHER INFORMATION: est
US-09-663-600A-45
Alignment Scores:
Pred. No.: 7.03e-114 Length: 1524
Score: 127.00 Matches: 228
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 2
Query Match: 55.22% Indels: 4
DB: Gaps: 0
US-09-787-677A-3 (1-230) x US-09-663-600A-45 (1-1524)
QY 1 MetAlaSerLeuGlnGlyLeuGlnValGlyTyrTyrLeuGlyLeuGlyLeuGly 20
Db 160 ATGGCCCTCTTGAGCTCCCACTGGGCTACATCTTACGCTTCTGGGCTTTGGGC 219
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrTyrThrSerSerTyrValGlyAlaSerIle 40
Db 220 ACACGTGTCCTGCTGCTGCTCCCACTGGAACAAGTTCTTATGCGGTGCAGCATT 279
QY 41 ValThrAlaValGlyPheSerIysGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 280 GTGACAGCAGTGGCTTCTTCCAGAGGCTCTGATGGAATGTCCACACACACAGGC 339
QY 61 IleThrGlnCyAspIleTyrSerThrLeuGlyLeuProAlaPheIleGln-AlaAl 80
Db 340 ATCACCCAGTGACATCTATACACCTTCTGCGCTGCGCTACATCCA-KCCTGC 398
QY 80 aglnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVa 100
Db 399 CCAAGCCATCATGTGTATCATCCAGTCATCTCTCCCTGCTGCTGATATCTGTGCT 458
QY 100 IglYmetArg-CyThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaVal 120
Db 459 GGGCATGAR-ATGCACAGCTTCTTCCAGGAATCCGAGCAACAGAGTGGCGTAG 517
QY 120 IagIyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTrpAsnL 140
Db 518 CAGGTGAGCTTTTTCATCTTGGAGGCTCTTGGATTCATTCCTGTTGCTGGATC 577
QY 140 euhIsglyIleLeuAAspPheTyrSerProLeuValProAspSerMetLysPheGluI 160
Db 578 TTCATGGATCCCAACGGAATCTTACTCACCACTGATGCTGACACATGAATTGAGA 637
QY 160 IegIyGlyAlaLeuTyrLeuGlyTyrIleIleSerSerLeuPheSerLeuIleAlaGlyT 180
Db 638 TTGAGAGGCTCTTCTTCTTGGGCAATATTCCTCCCTGTTCTCCGATGCTGGAATCA 697
QY 180 IeLeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGln 200
Db 698 TCCTCTGCTTTCTCTGCTATCCAGAGAAATGCTCACTACAGATGCTTACCAAG 757
QY 200 IagInProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSer 220
Db 758 CCAACCTCTTGCCACAGAGAGCTCTCCAGGCGCTGTAACCTCCCAAGTCAAGAGTG 817

Qy 220 IupheanSerTySerLeuThrGlyTyrVal 230
|||
Db 818 AGTTCATTCTCTACAGCTCAGAGGATATGTG 849

RESULT 4
US-09-252-991A-6070
; Sequence 6070, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/094,190

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6070

; LENGTH: 627
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6070

Alignment Scores:

Pred. No.: 10.1 Length: 627
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.91% Indels: 0
DB: 4 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-252-991A-6070 (1-627)

Qy 204 AlathrargSerSerProArgProGly 212
|||

Db 58 GCGACAGATCATCGCCCGGCTGGC 84

RESULT 5

US-09-252-991A-6398/c
; Sequence 6398, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6398

; LENGTH: 630
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6398

US-09-787-677A-3 (1-230) x US-09-252-991A-6398 (1-630)

Alignment Scores:

Pred. No.: 10.1 Length: 630
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.91% Indels: 0
DB: 4 Gaps: 0

Db 550 GCGACAGATCATCGCCCGGCTGGC 524

RESULT 6
US-09-252-991A-6226
; Sequence 6226, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6226

; LENGTH: 873
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6226

US-09-787-677A-3 (1-230) x US-09-252-991A-6226 (1-873)

Alignment Scores:

Pred. No.: 13.8 Length: 873
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.91% Indels: 0
DB: 4 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-252-991A-6226 (1-873)

Qy 204 AlathrargSerSerProArgProGly 212
|||

Db 320 GCGACAGATCATCGCCCGGCTGGC 346

RESULT 7

US-09-114-146-1
; Sequence 1, Application US/09114146
; Patent No. 6083747

; GENERAL INFORMATION:

; APPLICANT: MONG, Peter M.C.

; APPLICANT: HAN, Xiaodong
; TITLE OF INVENTION: GLYCOPROTEIN GP105 ON BLS HEMATOPOIETIC
; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/114,146

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/471,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 46074/102/FEIN

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-114-146-1

Alignment Scores:
Pred. No.: 62.5 Length: 410
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 3 Gaps: 0

US-09-787-677a-3 (1-230) x US-09-114-146-1 (1-410)

Qy 13 leuGlyLeuLeuGlyLeuLeuGly 20
Db 240 CTGGGCTGCTGGGCGCTGGGCG 263

RESULT 8
PCT-US96-08623-1
Sequence 1, Application PC/RUS9608623
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: GLYCOPROTEIN GP105 ON BLS HEMATOPOIETIC
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08623
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/471,188
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 46074/103/REIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US96-08623-1

Alignment Scores:
Pred. No.: 62.5 Length: 410
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 3 Gaps: 0

Query Match: 3.48% Indels: 0
DB: 5 Gaps: 0

US-09-787-677a-3 (1-230) x PCT-US96-08623-1 (1-410)

Qy 13 leuGlyLeuLeuGlyLeuLeuGly 20
Db 240 CTGGGCTGCTGGGCGCTGGGCG 263

RESULT 9
US-09-252-991A-257
Sequence 257, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIORITY FILING DATE: 1998-02-18
PRIORITY APPLICATION NUMBER: US 60/074,788
PRIORITY FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 257
LENGTH: 417
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-257

Alignment Scores:
Pred. No.: 63.5 Length: 417
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 4 Gaps: 0

US-09-787-677a-3 (1-230) x US-09-252-991A-257 (1-417)

Qy 70 leuLeuGlyLeuProAlaAspIle 77
Db 217 CTGCTGGGCTGCGCGCGACATC 240

RESULT 10
US-08-844-120-2
Sequence 2, Application US/08844120
Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Puri
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT19
CLONE: 2676650
US-08-844-120-2

Alignment Scores:
Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 2 Gaps: 0

US-09-787-677A-3 (1-230) x US-08-844-120-2 (1-709)

Qy 12 11leuG1yleuG1yleuG1yleu 19
Db 169 ATACTGGGCGCTGTAGGCGCTGT 192

RESULT 11
US-09-022-940-2
Sequence 2, Application US/092022940
Patent No. 5965423
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,940
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-022-940-2

Alignment Scores:
Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 2 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-022-940-2 (1-709)

Qy 12 11leuG1yleuG1yleuG1yleu 19
Db 169 ATACTGGGCGCTGTAGGCGCTGT 192

RESULT 13
US-09-213-394-2
Sequence 2, Application US/09213394

Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 2 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-022-940-2 (1-709)

Qy 12 11leuG1yleuG1yleuG1yleu 19
Db 169 ATACTGGGCGCTGTAGGCGCTGT 192

RESULT 12
US-09-216-386-2
Sequence 2, Application US/09216386
Patent No. 6093561
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-216-386-2

Alignment Scores:
Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 3 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-216-386-2 (1-709)

Qy 12 11leuG1yleuG1yleuG1yleu 19
Db 169 ATACTGGGCGCTGTAGGCGCTGT 192

RESULT 13
US-09-213-394-2
Sequence 2, Application US/09213394

Patent No. 6319701
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purni
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,394
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNOT19
CLONE: 2676650
US-09-213-394-2
Alignment Scores:
Pred. No.: 106 Length: 709
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 3 Gaps: 0
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QY 12 11lelenglyleuenglyleu 19
Db 169 ATCTGGGCTGTAGGCTGTTA 192
RESULT 14
US-09-252-991A-1683
Sequence 1683, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1683
LENGTH: 714
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1683
Alignment Scores:
Pred. No.: 107 Length: 714
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 4 Gaps: 0
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QY 204 AlathrArgSerProArgPro 211
Db 345 GCAACGAGATCTTCGCCAAGGCC 368
RESULT 15
US-09-270-767-1386
Sequence 1386, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1386
LENGTH: 753
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-1386
Alignment Scores:
Pred. No.: 112 Length: 753
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.48% Indels: 0
DB: 4 Gaps: 0
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Db 690 CGGTATCTCTCGACGAGGCA 713
Search completed: December 20, 2004, 21:25:57
Job time: 97 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 19:27:57 ; Search time 547 Seconds
(without alignments)
2321.376 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230
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Ygapop 60.0 , Ygapext 60.0
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4093002 seqs, 276041825 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8176338

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-TRANS=human0.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09787677 @CGN 1 1 480 @runcat.20122004.132820.19878
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Database :

Published Applications NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	230	100.0	1400	11	US-09-978-360A-56	Sequence 56, Appl
2	230	100.0	1400	10	US-10-319-763-139	Sequence 139, App
3	230	100.0	1475	10	US-09-888-257A-1	Sequence 1, Appl
4	230	100.0	1475	10	US-09-946-374-133	Sequence 133, App
5	230	100.0	1475	13	US-10-006-867-79	Sequence 79, Appl
6	230	100.0	1475	13	US-10-063-547-79	Sequence 79, Appl
7	230	100.0	1475	13	US-10-063-551-79	Sequence 79, Appl
8	230	100.0	1475	14	US-10-028-072-491	Sequence 491, App
9	230	100.0	1475	14	US-10-063-616-79	Sequence 79, Appl
10	230	100.0	1475	14	US-10-140-808-491	Sequence 491, App
11	230	100.0	1475	14	US-10-063-569-79	Sequence 79, Appl
12	230	100.0	1475	14	US-10-063-513-79	Sequence 79, Appl
13	230	100.0	1475	14	US-10-063-515-79	Sequence 79, Appl
14	230	100.0	1475	14	US-10-063-512-79	Sequence 79, Appl
15	230	100.0	1475	14	US-10-121-049-491	Sequence 491, App
16	230	100.0	1475	14	US-10-123-904-491	Sequence 491, App
17	230	100.0	1475	14	US-10-140-470-491	Sequence 491, App
18	230	100.0	1475	14	US-10-063-502-79	Sequence 79, Appl
19	230	100.0	1475	14	US-10-175-746-491	Sequence 491, App
20	230	100.0	1475	14	US-10-176-918-491	Sequence 491, App
21	230	100.0	1475	14	US-10-176-921-491	Sequence 491, App
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23	230	100.0	1475	14	US-10-137-865-491	Sequence 491, App
24	230	100.0	1475	14	US-10-140-474-491	Sequence 491, App
25	230	100.0	1475	14	US-10-142-431-491	Sequence 491, App
26	230	100.0	1475	14	US-10-143-114-491	Sequence 491, App
27	230	100.0	1475	14	US-10-140-002-491	Sequence 491, App
28	230	100.0	1475	14	US-10-063-554-79	Sequence 79, Appl
29	230	100.0	1475	14	US-10-006-856A-133	Sequence 133, App
30	230	100.0	1475	14	US-10-142-419-491	Sequence 491, App
31	230	100.0	1475	14	US-10-063-553-79	Sequence 79, Appl
32	230	100.0	1475	14	US-10-063-518-79	Sequence 79, Appl
33	230	100.0	1475	14	US-10-123-265-491	Sequence 491, App
34	230	100.0	1475	14	US-10-142-442-491	Sequence 491, App
35	230	100.0	1475	14	US-10-063-598-79	Sequence 79, Appl
36	230	100.0	1475	14	US-10-227-693-79	Sequence 79, Appl
37	230	100.0	1475	14	US-10-006-818A-133	Sequence 133, App
38	230	100.0	1475	14	US-10-121-050-491	Sequence 491, App
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40	230	100.0	1475	14	US-10-143-032-491	Sequence 491, App
41	230	100.0	1475	14	US-10-063-563-79	Sequence 79, Appl
42	230	100.0	1475	14	US-10-006-485A-133	Sequence 133, App
43	230	100.0	1475	14	US-10-013-907A-133	Sequence 133, App
44	230	100.0	1475	14	US-10-015-499A-133	Sequence 133, App
45	230	100.0	1475	14	US-10-063-555-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-978-360A-56
; Sequence 56, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas MiLine
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouguenel, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56, US4, CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563

PRIOR FILING DATE: 1998-04-13
 PRIOR APPLICATION NUMBER: US 60/096,116
 PRIOR FILING DATE: 1998-08-10
 PRIOR APPLICATION NUMBER: US 60/099,273
 PRIOR FILING DATE: -09-04
 PRIOR APPLICATION NUMBER: US 09/191,997
 PRIOR FILING DATE: 1998-11-13
 PRIOR APPLICATION NUMBER: US 09/215,435
 PRIOR FILING DATE: 1998-12-17
 PRIOR APPLICATION NUMBER: PCT/IB98/02122
 PRIOR FILING DATE: 1998-12-17
 PRIOR APPLICATION NUMBER: US 09/247,155
 PRIOR FILING DATE: 1999-02-09
 Remaining Prior Application data removed - See File wrapper or PALM.
 NUMBER OF SEQ ID NOS: 810
 SOFTWARE: Patent.pm
 SEQ ID NO 56
 LENGTH: 1400
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: sig.peptide
 LOCATION: 36..107
 OTHER INFORMATION: Von Heljne matrix
 OTHER INFORMATION: score 5.6999980926514
 OTHER INFORMATION: seq ILGLGLGLTIVA/ML
 FEATURE:
 NAME/KEY: polyA_signal
 LOCATION: 1302..1307
 FEATURE:
 NAME/KEY: polyA_site
 LOCATION: 1389..1400
 US-09-978-360A-56

Alignment Scores:

Pred. No.: 8,74e-218 Length: 1400
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-978-360A-56 (1-1400)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleuGlyLeuGlyLeuGly 20
 DB 36 ATGGCCCTCTTGCGCTCAACTGTGGCTACATCTTAGGCTTCTGGGGCTTTTGCGC 95
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerTlle 40
 DB 96 ACACGTGTTCCATGCTGCTGCCAGCTGGAACAAAGTTCTTATGTCGGTCCAGCAT 155
 QY 41 ValThrAlaValGlyPheSerTlleGlyLeuTyrMetGluCysAlaThrHisSerThGly 60
 DB 156 GTGACAGCAAGTGGCTTCTCCAGGGCTCTGATGAAATGTGCCACACACAGCAGGC 215
 QY 61 IleThGlnCysAspTlleTyrSerThrLeuGlyLeuProAlaAspTlleGlnAla 80
 DB 216 ATCAACCAAGTGTACATCTTAGCAACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCC 275
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 DB 276 CAGGCCATGATGGACATCTCAAGTCAATCTCTCTGCGCTCATTAATCTGTGTG 335
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120
 DB 336 GGCATGAGATGACACAGCTTCTGCGCAAGAAATCCGAGCAAAAGACAGATGGCGGTAGCA 395
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleThrAsnLeu 140
 DB 396 GGTGGAATCTTTTCATCTTGGAGGCTCTCTGGATTCATCTCTGTGCTTGGAAATCTT 455
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetTyrPheGluIle 160

DB 456 CATGGATCTCTAGGGAGCTTCTACTCACCAGCTGTGCTGACGATGAATTTGAGATT 515
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerIleuIleAlaGlyIleIle 180
 DB 516 GGAAGGCTCTTTCATCTTGGGCAATTAATTTCTTCCCTGTTCCTGTAGCTGAATCATC 575
 QY 181 LeuCyPheSerCysSerSerGlnArgAspArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 DB 576 CTCTGCTTTTCTGCTCATCTCCAGAAATCGCTCCAACTACTACATGCTTACCAAGCC 635
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIleValIleSerGlu 220
 DB 636 CAACCTTCTCCACAGAGACTCTCCAGAGCTGTGTCACCTCCAAAGTCAAGATGAG 695
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
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RESULT 2

US-10-319-763-139

Sequence 139, Application US/10319763
 Publication No. US2003014490A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Ducleert, Aymeric

APPLICANT: Bougueleret, Lydie

TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: G-031.US04.DIV

CURRENT APPLICATION NUMBER: US/10/319,763

CURRENT FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/069,957

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/074,121

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 60/081,563

PRIOR FILING DATE: 1998-04-13

PRIOR APPLICATION NUMBER: 60/096,116

PRIOR FILING DATE: 1998-08-10

PRIOR APPLICATION NUMBER: 60/099,273

PRIOR FILING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 229

SOFTWARE: Patent.pm

SEQ ID NO 139

LENGTH: 1400

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: sig.peptide

LOCATION: 36..107

OTHER INFORMATION: Von Heljne matrix

OTHER INFORMATION: score 5.6999980926514

OTHER INFORMATION: seq ILGLGLGLTIVA/ML

FEATURE:

NAME/KEY: polyA_signal

LOCATION: 1302..1307

FEATURE:

NAME/KEY: polyA_site

LOCATION: 1389..1400

US-10-319-763-139

Alignment Scores:

Pred. No.: 8,74e-218 Length: 1400
 Score: 230.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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US-09-787-677A-3 (1-230) x US-10-319-763-139 (1-1400)

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QY 21 ThrLeuValAlaMetLeuLeuProSerTTPlySerSerTyrValGlyAlaSerIle 40
DB 96 ACCTGTTGCCATGCTGCTCCAGCTGGAAAAACAAGTTCTTATGTCGGTGGCAGATT 155
QY 41 ValThrAlaValGlyPheSerLySGlyLeuTTPMeGlyCysAlaThrHisSerThrGly 60
DB 156 GTGACAGCAGTGGCTTCTCAAGGGCTCTGATGGAAATGTCACACACACAGCAGGC 215
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
DB 216 ATACACCAAGTATCACTATACACACCTTCTGGGCTTGGCCCTGACATCCAGGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 276 CAGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 335
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIlyAspArgValAlaVal 120
DB 336 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 395
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTTPAsnLeu 140
DB 396 GGTGAGGCTTTTTCATCTTGAAGGCTCTGGGATTCATCTTCTGCTGGAACTT 455
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
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QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerSerTyrTyrAspAlaTyrGlnAla 200
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RESULT 3

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US-09-888-257A-1
; Sequence 1, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Polakis, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5002R1
; CURRENT APPLICATION NUMBER: US/09/888, 257A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/063,540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/099,792
; PRIOR FILING DATE: 1998-09-10

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; PRIOR APPLICATION NUMBER: US 60/103,678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-888-257A-1
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Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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QY 21 ThrLeuValAlaMetLeuLeuProSerTTPlySerSerTyrValGlyAlaSerIle 40
DB 182 ACATGTTGCCATGCTGCTCCAGGCTGGAAAAACAAGTTCTTATGTCGGTGGCAGATT 241
QY 41 ValThrAlaValGlyPheSerLySGlyLeuTTPMeGlyCysAlaThrHisSerThrGly 60
DB 242 GTGACAGCAGTGGCTTCTTCCAGGCTCTGATGGAAATGTCACACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
DB 302 ATACACCAAGTATCACTATACACACCTTCTGGGCTTGGCCGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 362 CAGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIlyAspArgValAlaVal 120
DB 422 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTTPAsnLeu 140
DB 482 GGTGAGGCTTTTTCATCTTGAAGGCTCTGGGATTCATCTTCTGCTGGAACTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
DB 542 CAGGCATCTTACGGGACTTCTTACCACTGGTGTGCTGACATGAAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

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Db	602	GGAGAGGGCTTTACTTGGGACATTAATTCCTCCCTGTCTCCCTGATGATGGAATCATC	6611
Qy	181	LeuCyPheSerCysSerSerGlnIaGaaNAArgSerAenTyrTyrApaIaTyrGlnIaA	2000
Db	662	CTCTGCTTTTCTGTCTCATCCAGAAATAATCGCTCAACTACATACGATGCTTCAAGCC	7211
Qy	201	GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIysValIysSerGlu	2200
Db	722	CAACTCTTGGCCACAAGAGAGCTCTCCAAAGGCCCTGTGTCAACTCTCCAAAGTCAGAAGTGAAG	7611
Qy	221	PheAenSerTyrSerLeuThrGlyTyrVal	230
Db	782	TTCAATCTCTACAGCCTGACAGAGGTATGTG	811
RESULT 4			
US-09-946-374-133			
Sequence 133, Application US/09946374			
Publication No. US20030073129A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Botstein, David			
APPLICANT: Desnoyers, Luc			
APPLICANT: Eaton, Dan L.			
APPLICANT: Ferrara, Napoleone			
APPLICANT: Fong, Sherman			
APPLICANT: Gao, Wei-Qiang			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Grimaldi, Christopher J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Hillan, Kenneth J.			
APPLICANT: Pan, James			
APPLICANT: Paoni, Nicholas F.			
APPLICANT: Roy, Margaret Ann			
APPLICANT: Smith, Victoria			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumas, Daniel			
APPLICANT: Watanabe, Colin K.			
APPLICANT: Williams, P. Mickey			
APPLICANT: Wood, William I.			
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
TITLE OF INVENTION: Acids Encoding the Same			
FILE REFERENCE: P2830P1C1			
CURRENT APPLICATION NUMBER: US/09/946,374			
CURRENT FILING DATE: 2001-09-04			
PRIOR APPLICATION NUMBER: 60/098716			
PRIOR FILING DATE: 1998-09-01			
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PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores: 9.17e-218 Length: 1475
Pred. No.:

Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-787-677a-3 (1-230) x US-09-946-374-133 (1-1475)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 122 ATGGCTCTCTTGGCTCCCACTTGGGCTAATCTTGGGCTTGGGCTTGGGCT 181
QY 21 ThrLeuValAlaMetLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
DB 182 ACACGTGTCCCAAGTCTCCCACTGCAAAACAGTCTTATGTCGTGCGAGCAT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
DB 242 GTACACAGCACTTGGCTTCTCCAAAGGCTCTGATGGATGTCCACACACACAGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
DB 302 ATCACCAGTGTACATCTATACACCTTCTGGCTGCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 362 CAGGCATGATGTGATGCATCCAGTGCATCTCTCCCTGCGCTGATCTCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaAla 120
DB 422 GGCATAGATGCACATCTTCTCCAGGAATCCAGCAACAGAGTGGCGTACGA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrPheLeu 140
DB 482 GGTGGAGTCTTTTCTCTCTGAGGCTCTGAGGATTCCTCTTGGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
DB 542 CATGGATCTCTAGGAGCTTACTACCACTGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GAGAGGCTCTTACTCTGGCATTAATTTCTCTCTCTCTGATGTAATCATC 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCTGCTTTTCTGCTCATCTCCAGAAATCGCTCCAACTAAGATGCTTCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValIleSerGlu 220
DB 722 CAACCTCTTGCCCAAGAGCTCTCCAAAGCTGTCAACCTTCCAAAGTCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAAATTCCTACAGCTGTACAGGATATGTG 811
RESULT 5
US-10-006-867-79
; Sequence 79, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1

CURRENT APPLICATION NUMBER: US/10/006,867
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29
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PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
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Alignment Scores:

Pred. No.:	9,17e-218	Length:	1475
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-787-677a-3 (1-230) x US-10-006-867-79 (1-1475)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 122 ATGGCTCTCTTGGCTCCCACTTGCTGCTACATCTTGGGCTTGGGGCTTTGGG 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerTyrValGlyAlaSerIle 40
DB 182 ACCTGCTTGGCCATGCTGCTCCCACTGGAAGAAAGTTCTTATGCGGTGCACGATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 242 GTACACGACATTGGCTTCTCCAGGGCTCTGATGGAATGTGCCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 302 ATCACCAGGTGACATCTATAGACCCCTTCTGGGCTGCGCGTGCATCCAGGCTGCC 361
QY 81 GlnAlaMetMetAlaThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGATGATCATCAGGCAATCTCTCCCTGCGCTGCATTAATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIlysaAspArgValAlaValAla 120
DB 422 GGCATAGATGACACAGTCTTCTGCGAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCA 481
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QY 121 GlyIleValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
DB 482 GTGGAGCTCTTTTTCATCTTGAGGCTCTCGGATTAATCTGTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGAGACTTCTATCTACACCTGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GGAGAGCTCTTACTTGGGCAATTAATTTCTTCCCTGCTCCTGATAGCTGAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTrpAspAlaTyrGlnAla 200
DB 662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATGCTCCAACTACATACATGCTTACCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTCTTCCCAAGAGACTTCCAGGCTGTGTCAACCTCCCAAGTCAAGAGTGAAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAATTCTACAGGCTGACAGGATATGTG 811
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RESULT 6

US-10-063-547-79
Sequence 79, Application US/10063547
Publication No. US20020182638A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien

US-10-063-547-79

Alignment Scores:

Pred. No.:	9,17e-218	Length:	1475
Score:	230.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-787-677a-3 (1-230) x US-10-063-547-79 (1-1475)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 122 ATGGCTCTCTTGGCTCCCACTTGCTGCTACATCTTGGGCTTGGGGCTTTGGG 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerTyrValGlyAlaSerIle 40
DB 182 ACCTGCTTGGCCATGCTGCTCCCACTGGAAGAAAGTTCTTATGCGGTGCACGATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 242 GTACACGACATTGGCTTCTCCAGGGCTCTGATGGAATGTGCCACACACAGCAGGC 301
```

QY 61 ILeThGInCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
| | | | |
Db 302 ATCAACCCAGGTGATGACATCTTAGCACCCCTCTGGAGCTGCGGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAla 100
| | | | |
Db 362 CAGGCCATGATGGATGACATCCAGTCAATCTCCCTGGCTGTCATTTCTCTGTGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAlaValAlaAla 120
| | | | |
Db 422 GGCATGAGATGACACAGCTCTCTGCCAGAAATCCGACCAAGCAAGATGGCGGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIlePheValAlaAlaTrpAsnLeu 140
| | | | |
Db 482 GGTGAGATCTTTTTCATCTTGGAGGCTCTGGGATTCATCTCTGTGGTGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
| | | | |
Db 542 CATGGATCTCAAGGACTTCTACTCAACACTGGTGGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlnAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
| | | | |
Db 602 GGAAGGCTCTTTACTGGGCTATTTCTTCCCTGTCTCCGTAGATGCTGGATCATC 661
QY 181 LeuCyAPheserCysSerSerGlnArgAsnArgSerAsnTyTyTrpAspAlaTyGlnAla 200
| | | | |
Db 662 CTCGCTTTTCTCTCTCATCTCCAGAGAAATGCTCCACATCTACATGCTTCAAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
| | | | |
Db 722 CAACCTCTTGCCACAGAGACTCTCCAAAGGCTGTGTCACCTCCCAAGTCAAGAGTGGAG 781
QY 221 PheAsnSerTySerLeuThrGlyTyVal 230
| | | | |
Db 782 TTCATTCTTACAGCTGACAGGGGTATGTG 811

RESULT 7

US-10-063-551-79
; Sequence 79, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eacon, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-79

Alignment Scores:

Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-551-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyTrilleuGlyLeuLeuGlyLeuLeuGly 20
| | | | |
Db 122 ATGGCCCTCTTGGCTCCCAACTTGGGCTTACATCTAGAGCTTCTGGGCTTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
| | | | |
Db 182 ACATGGTTCCATGCTGCTCCCAAGTGAAGAAACAAGTTCTTATGCGGTGCAGCATT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysAlaAlaThrHisSerTrnGly 60
| | | | |
Db 242 GTACAGACATTTGGCTTCTCCAAAGGCTCTGTGATGAAATGTCACACACAGCAGGC 301
QY 61 ILeThGInCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
| | | | |
Db 302 ATCAACCCAGGTGATGACATCTTAGCACCCCTCTGGAGCTGCGGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAla 100
| | | | |
Db 362 CAGGCCATGATGGATGACATCCAGTCAATCTCCCTGGCTGTCATTTCTCTGTGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAlaValAlaAla 120
| | | | |
Db 422 GGCATGAGATGACACAGCTCTCTGCCAGAAATCCGACCAAGCAAGATGGCGGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIlePheValAlaAlaTrpAsnLeu 140
| | | | |
Db 482 GGTGAGATCTTTTTCATCTTGGAGGCTCTGGGATTCATCTCTGTGGTGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
| | | | |
Db 542 CATGGATCTCAAGGACTTCTACTCAACACTGGTGGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyGlnAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
| | | | |
Db 602 GGAAGGCTCTTTACTGGGCTATTTCTTCCCTGTCTCCGTAGATGCTGGATCATC 661
QY 181 LeuCyAPheserCysSerSerGlnArgAsnArgSerAsnTyTyTrpAspAlaTyGlnAla 200
| | | | |
Db 662 CTCGCTTTTCTCTCTCATCTCCAGAGAAATGCTCCACATCTACATGCTTCAAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
| | | | |
Db 722 CAACCTCTTGCCACAGAGACTCTCCAAAGGCTGTGTCACCTCCCAAGTCAAGAGTGGAG 781
QY 221 PheAsnSerTySerLeuThrGlyTyVal 230
| | | | |
Db 782 TTCATTCTTACAGCTGACAGGGGTATGTG 811

RESULT 8

US-10-028-072-491
; Sequence 491, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
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PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077921
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
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PRIOR APPLICATION NUMBER: 60/085339
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
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PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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Alignment Scores:

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Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
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US-09-787-677a-3 (1-230) x US-10-028-072-491 (1-1475)

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Qy 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlnLeuGlyLeuLeuGly 20
Db 122 ATGGCCCTCTTGCCCTTCACTTGAGGCTACATCTTAGGCTTCTGGGCTTTTGGC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 182 ACACTGTTGCATGCTGCTCCAGCTGGAACCAAGTTCTTATGCGGTGCCAGCAT 241
Qy 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaIleThrHisSerThGly 60
Db 242 GTGCACACAGTTGGCTTCTCCAGGCGCTCTGATGATGTGCACACACAGCAGGC 301
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlnLeuProAlaAspIleGlnAla 80
Db 302 ATACCCAGTGTGATCTATAGCACCCCTTCTGGGCTGCGCCGTGACATCCAGGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCGCATGATGAGCATCTCAGTCAATCCCTCCGCGCTCATATTATCTGTGTG 421
Qy 101 GlyMetArgCysThrValPheCysGlnGlnSerAlaGlyAlaValAlaValAla 120
Db 422 GGCGTGTGATGACACAGTCTTCTCCAGGAAATCCGAGCAAAAGACAGTGGCGGTGCA 481
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTrpAsnLeu 140
Db 482 GGTGTGAGCTTTTTCATCTTGAGGCTCTCTGAGATTCATCTCTGTGCTGGAATCTT 541
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
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Db 542 CATGGATCTCAAGGACTTCTACTCACACAGTGTGCTGACAGCATGAATTTGAGATT 601
Qy 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGGCTCTTACTTGAGCATTTATTTCTCTGTTCTCCGTGATGCTGGAATCATC 661
Qy 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTCCGCTCATCTCCAGAAATCGCTCCAACTACTACATGCTTCCAAAGCC 721
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db 722 CAACCTCTTCCCAAGAGACTCTCCAAAGGCTGTGTCAACTCTCCAAAGTCAAGAGAG 781
Qy 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATTTCTTACAGCTTGACAGGGATG 811
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RESULT 9

US-10-063-616-79

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; Sequence 79, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
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; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
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US-10-063-616-79

Alignment Scores:

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Pred. No.: 9,17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
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US-09-787-677a-3 (1-230) x US-10-063-616-79 (1-1475)

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Qy 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlnLeuGlyLeuLeuGly 20
Db 122 ATGGCCCTCTTGCCCTTCACTTGAGGCTACATCTTAGGCTTCTGGGCTTTTGGC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db 182 ACACTGTTGCATGCTGCTCCAGCTGGAACCAAGTTCTTATGCGGTGCCAGCAT 241
Qy 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaIleThrHisSerThGly 60
Db 242 GTGCACACAGTTGGCTTCTCCAGGCGCTCTGATGATGTGCACACACAGCAGGC 301
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuGlnLeuProAlaAspIleGlnAla 80
Db 302 ATACCCAGTGTGATCTATAGCACCCCTTCTGGGCTGCGCCGTGACATCCAGGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-79

Alignment Scores:
Pred. No.:      9,17e-218      Length:      1475
Score:          230.00         Matches:      230
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%        Indels:       0
DB:             14             Gaps:         0

US-09-787-677a-3 (1-230) x US-10-063-569-79 (1-1475)

QY      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db      122 ATGGCCCTCTTGCCCTCCCACTGTGGGCTACATCTTAGGCCCTTCTGGGGCTTTTGCGC 181

QY      21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db      182 ACCTGCTTCCATGCTGCTCCCACTGGAAACAAAGTTCTTATGTCGGTCCAGCATTT 241

QY      41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db      242 GTGACAGCAGTGGCTTCTCCAAAGGCTCTGATGGATGTGCACACACAGCAGCAGGC 301

QY      61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db      302 ATACCCAGGTGACATCTATAGCACCCTTCTGGGCTGCGCGTGAATCCAGGCTGCC 361

QY      81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db      362 CAGGCCATGATGGATGACATCAGATCAGCAATCTCTCCCTGGGCTGATTAATCTGTGTG 421

QY      101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db      422 GGCATGAGATGACAGCTTCTCCAGGAAATCCGAGCAAAAGACAGATGGCGGTAGCA 481

QY      121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTrpAsnLeu 140
Db      482 GGTGGATCTTTTTCATCTTGAGGCTCTGAGGATTCATCTGTGCTGCTGGAATCTT 541

QY      141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db      542 CAGGATCTCTTACGGGACTTCTACTCACACTGTGCTGACACAGCAAGAAATTTGAATTT 601

QY      161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GGAAGGCTCTTACTTGGGCAATTAATTTCTTCCCTGTTCTCCGTGATAGTGAATCATC 661

QY      181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaIleTyrGlnAla 200
Db      662 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTAATAGATGCTTACCAAGCC 721

QY      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
Db      722 CAACCTTTTCCACAGAGAGCTCTCCAAAGGCTGTCAACTCCCAAGTCAAGAGTGAAG 781

QY      221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db      782 TTCAATTCTTACAGCTGACAGGATATGTG 811

RESULT 12
US-10-063-513-79
; Sequence 79, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```

; APPLICANT: Gueney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; PRIORITY FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-79

Alignment Scores:
Pred. No.:      9,17e-218      Length:      1475
Score:          230.00         Matches:      230
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%        Indels:       0
DB:             14             Gaps:         0

US-09-787-677a-3 (1-230) x US-10-063-513-79 (1-1475)

QY      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db      122 ATGGCCCTCTTGCCCTCCCACTGTGGGCTACATCTTAGGCCCTTCTGGGGCTTTTGCGC 181

QY      21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
Db      182 ACCTGCTTCCATGCTGCTCCCACTGGAAACAAAGTTCTTATGTCGGTCCAGCATTT 241

QY      41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db      242 GTGACAGCAGTGGCTTCTCCAAAGGCTCTGATGGATGTGCACACACAGCAGCAGGC 301

QY      61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db      302 ATACCCAGGTGACATCTATAGCACCCTTCTGGGCTGCGCGTGAATCCAGGCTGCC 361

QY      81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db      362 CAGGCCATGATGGATGACATCAGATCAGCAATCTCTCCCTGGGCTGATTAATCTGTGTG 421

QY      101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db      422 GGCATGAGATGACAGCTTCTCCAGGAAATCCGAGCAAAAGACAGATGGCGGTAGCA 481

QY      121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTrpAsnLeu 140
Db      482 GGTGGATCTTTTTCATCTTGAGGCTCTGAGGATTCATCTGTGCTGCTGGAATCTT 541

QY      141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db      542 CAGGATCTCTTACGGGACTTCTACTCACACTGTGCTGACACAGCAAGAAATTTGAATTT 601

QY      161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db      602 GGAAGGCTCTTACTTGGGCAATTAATTTCTTCCCTGTTCTCCGTGATAGTGAATCATC 661

QY      181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaIleTyrGlnAla 200
Db      662 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTAATAGATGCTTACCAAGCC 721

QY      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
Db      722 CAACCTTTTCCACAGAGAGCTCTCCAAAGGCTGTCAACTCCCAAGTCAAGAGTGAAG 781

QY      221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db      782 TTCAATTCTTACAGCTGACAGGATATGTG 811
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RESULT 13
US-10-063-515-79
; Sequence 79, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-515-79

Alignment Scores:
Pred. No.: 9, 17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-09-787-677a-3 (1-230) x US-10-063-515-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
DB 122 ATGGCTCTCTGGCTCCCAACTGTGGCTACATCTTAGGCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValAlaSerIle 40
DB 182 ACCTGCTGTGCGCATGCTGCTCCCACTGGAAGAAACAAGTTCTTAATGCGGTGCGAGCATT 241
QY 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 242 GTACACGACGCTTGGCTTCTCCAGGGGCTCTGATGGAATGTGCCACACAGCACAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 302 ATCACCAAGGTGACATCTATAGCAACCTCTGGGCTGCGCGGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGTGTGATCATCAGTGCATCTCCCTGCGCTGACATTAATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
DB 422 GGCATAGATGACACAGTCTTCTCCAGAGATCCCGACCAAGACAGAGTGGCGGTAGCA 481
QY 121 GlyGlyValAlaPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
DB 482 GGTGGAGTCTTTTCACTCTTGGAGGCTCTGGGATTCATTCCTGTGCTGGAAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
DB 542 CATGGATCTTACGGGACCTTCTACTCACTGCTGCTTCAAGCATGAATAATTGAAATT 601
QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
DB 602 GGAGAGGCTCTTAATCTTGGGCAATTAATTTCTTCCCTGTTCTCCTGATAGCTGAATCATC 661
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QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTrpAspAlaTyrGlnAla 200
DB 662 CTCCTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTACTACATGCTTACCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTTGGCCCAAGAGAGCTCTCCAGGCTGTGTCACCTGCCAAAGTCAGAGATGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAATTCCTACAGCTGACAGGATATGTG 811

RESULT 14
US-10-063-512-79
; Sequence 79, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-79

Alignment Scores:
Pred. No.: 9, 17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-09-787-677a-3 (1-230) x US-10-063-512-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
DB 122 ATGGCTCTCTGGCTCCCAACTGTGGCTACATCTTAGGCTTGGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValAlaSerIle 40
DB 182 ACCTGCTGTGCGCATGCTGCTCCCACTGGAAGAAACAAGTTCTTAATGCGGTGCGAGCATT 241
QY 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 242 GTACACGACGCTTGGCTTCTCCAGGGGCTCTGATGGAATGTGCCACACAGCACAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 302 ATCACCAAGGTGACATCTATAGCAACCTCTGGGCTGCGCGGTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGTGTGATCATCAGTGCATCTCCCTGCGCTGACATTAATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
DB 422 GGCATAGATGACACAGTCTTCTCCAGAGATCCCGACCAAGACAGAGTGGCGGTAGCA 481
```

QY 121 G1YGLVAlaPhePheIleLeuGlyIleuLeuGlyPheIleProVala1aTPaenLeu 140
DB 482 GGTGGAGCTCTTTCATCTTGAGGCTCTCGGATTCATCTGTTGGCTGGAATCTT 541
QY 141 H1G1Y1leuAArgAaPheTYrSerProLeuVala1ProAaSerMeLysPheGluIle 160
DB 542 CARGGATCTTACGGGACTTCTACTCACACTGGTGTGCTGACAGCAAGAAATTTGAATT 601
QY 161 G1YGLuAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIlealagIY1leIle 180
DB 602 GGAGAGGCTCTTACTTGGGCAATTAATTCCTGTTCTCCCTGATAGCTGGAATCATC 661
QY 181 LeuCyPheSerCySerSerGlnArgAaArgSerAntTYrTYrAaPa1aTYrGlnAla 200
DB 662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 721
QY 201 G1nProLeuAlaThraArgSerSerProArgProGlyGlnProPolysVala1LysSerGlu 220
DB 722 CAACCTCTTGCACAGAGACTCTCCAAAGGCTGTGTCACTCCCAAGTCAGAGTGTGAG 781
QY 221 PheaAaSerTYrSerLeuThrgIYTYrVal 230
DB 782 TTCATTCCTACAGCTGACAGGCTATGTG 811
RESULT 15
US-10-121-049-491
Sequence 491, Application US/10121049
Publication No. US2003002239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Guiney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 491
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-121-049-491

Alignment Scores:

Prod. No.: 9.17e-218 Length: 1475
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-121-049-491 (1-1475)

QY 1 Meta1aSerLeuGlyLeuGlnLeuVala1YTYrIleLeuGlyLeuLeuGlyLeuLeuGly 20
DB 122 ATGGGCTCTTGGCTCCAACTGTGGGCTACATCTTCCAGGCTTTCGGGCTTTGGGC 181

QY 21 ThrLeuVala1aMetLeuLeuProSerTrpLysThrSerSerTYrVala1aIleSerIle 40
DB 182 ACATGCTTCCATTCGCTGCTCCCACTGGAAGAAACAAAGTTCTTATGCTGGTCCAGCATT 241
QY 41 ValThraVala1aGlyPheSerLysGlyLeuTrpMetGluCysa1aThraHisSerThrgIY 60
DB 242 GTGACAGCACTTGGCTTCTCCAAAGGCTCTGGATGGAATGTCCACACACAGCAGGCTG 301
QY 61 IleThrgInCysaPheIleTYrSerThrLeuGlyIleuProAlaAaPheIleGlnAla 80
DB 302 ATCACCCAGGTGACACATCTTACACACCTTCTGGGCTGTGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetLeuVala1ThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVala1 100
DB 362 CAGGCAAGATGAGTACATCACTGACATCAATTCCTCCCTGAGCTGATTAATCTGTGTG 421
QY 101 GlyMetArgCysThraVala1PheCysGlnGlnSerArgAlaLysAaPaVa1aVala1a 120
DB 422 GGATGAGATGACACAGCTCTTCCAGAGATCCCGAGCAAGAGAGTGGGCTGCA 481
QY 121 G1YGLVAlaPhePheIleLeuGlyIleuLeuGlyPheIleProVala1aTPaenLeu 140
DB 482 GGTGGAGCTCTTTCATCTTGAGGCTCTCGGATTCATTCCTGTTGCTGGATCTT 541
QY 141 H1G1Y1leuAArgAaPheTYrSerProLeuVala1ProAaSerMeLysPheGluIle 160
DB 542 CARGGATCTTACGGGACTTCTACTCACACTGGTGTGCTTACAGCATGAATTTGAATT 601
QY 161 G1YGLuAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIlealagIY1leIle 180
DB 602 GGAGGCTCTTACTTGGGCAATTAATTCCTGTTCTCCCTGATAGCTGGAATCATC 661
QY 181 LeuCyPheSerCySerSerGlnArgAaArgSerAntTYrTYrAaPa1aTYrGlnAla 200
DB 662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 721
QY 201 G1nProLeuAlaThraArgSerSerProArgProGlyGlnProPolysVala1LysSerGlu 220
DB 722 CAACCTCTTGCACAGAGACTCTCCAAAGGCTGTGTCACTCCCAAGTCAGAGTGTGAG 781
QY 221 PheaAaSerTYrSerLeuThrgIYTYrVal 230
DB 782 TTCATTCCTACAGCTGACAGGCTATGTG 811

Search completed: December 20, 2004, 21:38:46
Job time : 551 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 17:55:02 ; Search time 3199 Seconds
(without alignments)
2619.924 Million cell updates/sec

Title: US-09-787-677A-3
Perfect score: 230
Sequence: 1 MASLSGLVGYITGLLGLG.....PGQPKVKSFRNSYLTGY 230

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 1

Total number of hits satisfying chosen parameters: 65644297

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O/cgml 1/USPTO.spool/US09787677/rnat 20122004.132817.19771/app.query.fasta_1.391
-DB=EST -OEMT=fastap -SUPFIX=oli.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09787677 @CGN 1.1 3437 @rnat 20122004.132817.19771 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:.*
1: gb_est1:.*
2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_gsa1:.*
9: gb_gsa2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	693	9 AY400251	AY400251 Homo sapi
2	208	90.4	693	9 AY400252	AY400252 Pan trogl
3	195	84.8	680	2 BE304667	BE304667 601105783
4	191	83.0	822	4 BG386074	BG386074 602455248
5	179	77.8	728	4 BG325755	BG325755 602424466
6	171	74.3	650	7 CR546700	CR546700 DKF2P470L
7	171	74.3	652	7 CR628947	CR628947 DKF2P469L
8	155	67.4	978	4 BG164062	BG164062 602341087
9	153	66.5	494	4 BG385562	BG385562 602453858

10	124	53.9	945	2 BE513091	BE513091 601171545
11	122	53.0	570	7 CR628828	CR628828 DKF2P469B
12	119	51.7	758	6 CB999779	CB999779 AGENCOURT
13	113	49.1	459	6 CA389170	CA389170 cs06d06.y
14	111	48.3	421	7 CR554772	CR554772 DKF2P469E
15	110	47.8	560	1 AI953481	AI953481 wq29b02.x
16	79	34.3	643	4 BG328625	BG328625 602427889
17	74	32.2	359	7 TB6266	TB6266 y084t07.r1
18	64	27.8	866	2 BF032123	BF032123 601559727
19	59	25.7	655	7 CR975368	CR975368 4106492 B
20	59	25.7	761	5 BP445902	BP445902 BP445902
21	58	25.2	403	1 AI16661	AI16661 ue28a02.y
22	58	25.2	437	6 CB790981	CB790981 AGMNCIC.C
23	58	25.2	458	2 BF789570	BF789570 602103665
24	58	25.2	470	7 CK392258	CK392258 K0843808-
25	58	25.2	496	6 CA885318	CA885318 B0117804-
26	58	25.2	520	1 AI746647	AI746647 u101904.y
27	58	25.2	564	6 BY705200	BY705200 BY705200
28	58	25.2	593	1 AI789119	AI789119 u51c01.y
29	58	25.2	648	7 CK390708	CK390708 K0822D03-
30	58	25.2	659	1 AI789490	AI789490 UK99h03.y
31	58	25.2	763	9 AY400253	AY400253 Mus muscu
32	58	25.2	704	4 BI330754	BI330754 602982419
33	58	25.2	727	4 BI101652	BI101652 602887470
34	58	25.2	736	5 BM951102	BM951102 UT-M-EH0-
35	58	25.2	738	6 CA467958	CA467958 AGENCOURT
36	58	25.2	750	6 AW475316	AW475316 un64d02.y
37	58	25.2	752	6 CB955500	CB955500 AGENCOURT
38	58	25.2	754	7 CK129571	CK129571 AGENCOURT
39	58	25.2	762	7 CK021120	CK021120 AGENCOURT
40	58	25.2	774	7 CK031415	CK031415 AGENCOURT
41	58	25.2	777	4 BI102100	BI102100 602887847
42	58	25.2	786	8 B2215522	B2215522 CH230-416
43	58	25.2	787	2 BF781962	BF781962 602106220
44	58	25.2	818	6 CA469360	CA469360 AGENCOURT
45	58	25.2	896	6 CA492032	CA492032 AGENCOURT

ALIGNMENTS

RESULT 1
AY400251
LOCUS
DEFINITION
Homo sapiens CLDN2 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION
AY400251.1 GI:39756240
VERSION
GSS.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
REFERENCE
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
1 (bases 1 to 693)
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 693)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
location/Qualifiers
1..693

/clone_1lb="NIH MGC 15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies) "

ORIGIN

Alignment Scores:

Pred. No.:	6,79e-176	Length:	822
Score:	191.00	Matches:	191
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	83.04%	Indels:	0
DB:	4	Gaps:	0

US-09-787-677a-3 (1-230) x BG386074 (1-822)

QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleuGlyLeuGlyLeuGly 20
127 ATGGCTCTCTGGCTCCAACTGTGGCTACATCTAGGCTTGTGGGCTTTGGGC 186
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLyThrSerSerTyrValGlyAlaSerIle 40
187 ACACTGGTTCAGACGCTCCAGCTGAGAAACAAGTTTATGTCGGGCGACGATTT 246
QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrHisSerThgIy 60
247 GTACAGCAAGTGGCTTCTCCAGGCTCTCGATGGAATGTGCACACAGCACAGGCG 306
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
307 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCAGGCTGCC 366
QY 81 GlAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
367 CAGGCCATGATGGAGAACATCCAGTCAATCTCCCTCGGCTCATTAATCTGTGGTG 426
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIlyAspArgValAlaValAla 120
427 GGCATGATGATGACAGCTTCTGTCCAGGAATCCGAGCAAGAGTGGCGTGCA 486
QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTrpAsnLeu 140
487 GGTGAGCTCTTTTCATCTGTGAGGCTCTCGGATTCATTCCTGTGCTGGAATCTT 546
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlyPheGluIle 160
547 CATGGATCTCAGCGACTTCTACTACCACTGGTGGCTGACACAGAAATTTGAGATT 606
QY 161 GlyIleValAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
607 GGAGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCCTCGATGACGGAATCATC 666
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArg 191
667 CTCTGCTTTTCTGCTCATCCAGAGAAATCGT 699
Db

RESULT 5

BG325755

LOCUS BG325755 728 bp mRNA linear EST 27-FEB-2001
DEFINITION 60242446F1 NIH MGC_14 Homo sapiens cDNA clone IMAGE:4562273 5',
mRNA sequence.

ACCESSION

BG325755

VERSION

BG325755.1 GI:13132179

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 728)
AUTHORS NIH-MGC <http://imgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strauberg, Ph.D.
Email: csgrbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Sequencing: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LICM274 row: d column: 18
High quality sequence stop: 708.
Location/Qualifiers

FEATURES

source

1. 728
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4562273"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 14"
/note="Organ: Kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies) "

ORIGIN

Alignment Scores:

Pred. No.:	3.22e-164	Length:	728
Score:	179.00	Matches:	196
Percent Similarity:	99.49%	Conservative:	0
Best Local Similarity:	99.49%	Mismatches:	1
Query Match:	77.83%	Indels:	1
DB:	4	Gaps:	0

US-09-787-677a-3 (1-230) x BG325755 (1-728)

QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleuGlyLeuGlyLeuGly 20
30 ATGGCTCTCTGGCTCCAACTGTGGCTACATCTAGGCTTGTGGGCTTTGGGC 88
Db

QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLyThrSerSerTyrValGlyAlaSerIle 40
89 ACACTGGTTCAGACGCTCCAGCTGAGAAACAAGTTTATGTCGGGCGACGATTT 148
Db

QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrHisSerThgIy 60
149 GTGACACAGTGGCTTCTCCAGGCGCTCGATGGAATGTGCACACAGCAGCAGGC 208
Db

QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
209 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCAGGCTGCC 268
Db

QY 81 GlAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
269 CAGGCCATGATGGAGAACATCCAGTCAATCTCCCTCGGCTCATTAATCTGTGGTG 328
Db

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIlyAspArgValAlaValAla 120
329 GGCATGATGATGACAGCTTCTGTCCAGGAATCCGAGCAAGAGTGGCGTGCA 388
Db

QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTrpAsnLeu 140
389 GGTGAGCTCTTTTCATCTGTGAGGCTCTCGGATTCATTCCTGTGCTGGAATCTT 448
Db

QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlyPheGluIle 160

Db 449 CATGGATCTTACGGGACTTCTACTCACCTGATGCTTACACAGCAATTTGAGATT 508
 |||
 Qy 161 G1yG1uAlaLeuTyrlLeuGlylleleSerSerleuPheSerleuilealaglylle 180
 |||
 Db 509 GGAGAGCTCTTACTGCGGATATTCTTCCCTGTTCTCCGATAGCTGGAAATCATC 568
 |||
 Qy 181 LeuCyPheSerCySerSerGlnArgAbaArgSerAntyTyraapa 197
 |||
 Db 569 CTCTGCTTTCTGCTCATCTCCAGAGAAATGCTCCAACTACTGATGCT 619
 |||
 RESULT 6
 CR546700 650 bp mRNA linear EST 07-JUL-2004
 LOCUS DKEZp470L1824_r1.470 (synonym: pliv1) Pongo pygmaeus cDNA clone
 DKEZp470L1824_5', mRNA sequence.
 ACCESSION CR546700
 VERSION CR546700.1 GI:49899227
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 1 (bases 1 to 650)
 Wambutt, R., Heubner, D., Mewes, H.W., Well, B., Amid, C., Oeanger, A.,
 Fobo, G., Han, M. and Wiemann, S.
 Pongo pygmaeus mRNA (Wambutt, R., Heubner, D., Mewes, H.W., et al.)
 Unpublished (2004)
 TITLE Pongo pygmaeus mRNA (Wambutt, R., Heubner, D., Mewes, H.W., et al.)
 JOURNAL
 COMMENT
 CONTACT: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKF2);
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Agowa
 (Berlin/Germany) within the cDNA sequencing consortium of the
 German Genome Project. This clone (DKEZp470L1824) is available at
 the RZPD in Berlin. Please contact the RZPD: Ressourcentrum,
 Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email:
 clone@rzpd.de Further information about the clone and the
 sequencing project is available at
 http://mips.gsf.de/projects/cdna/.
 FEATURES
 source
 location/Qualifiers
 1..650
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKEZp470L1824"
 /issue_type="liver"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1b="470 (synonym: pliv1)"
 /note="Vector: pSport1_Sfi, Site_1: SfiIA, Site_2: SfiIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.89e-156 Length: 650
 Score: 171.00 Matches: 171
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.35% Indels: 0
 DB: 7 Gaps: 0
 US-09-787-677A-3 (1-230) x CR546700 (1-650)
 Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrlLeuGlyLeuGlyLeuGly 20
 |||
 Db 137 ATGGCTCTCTTGGCTCCCACTGTGGGCTACTGAGCTTCTGGGCTTTGGGC 196
 |||
 Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyraValaSerile 40
 |||
 Db 197 ACACGTGCTGCATGCTGCTCCAGCTGGAAAACAAGTTCTTACGTCGGGCGACGATT 256
 |||
 Qy 41 ValThrAlaValaGlyPheSerLysGlyLeuTrpMetGlnCybaIatThrLysSerThrgly 60
 |||

Db 257 GTGACACAGCTTGAGCTTCTCCAGAGGCTTGGATGAGTGTGACACAGACAGCT 316
 |||
 Qy 61 IleThrGlnCybaPheLysSerThrLeuGlyLeuProAlaapPileglnAla 80
 |||
 Db 317 ATGACCCAGTGTACATCTATACACACCTTCTGGGCTGCGCCGTGACATCCAGGCTGCC 376
 |||
 Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
 |||
 Db 377 CAGGCGCATGTGTGATCATCATCATGCAATCTCTCCCTGCGCTGCATTAATCTGTGGTG 436
 |||
 Qy 101 G1yMetArgCySerThrValPheCyGlnGlnUserArgAlaYsaPaValaVala 120
 |||
 Db 437 GGATGAGATGACAGCTTCTCCAGAGAAATCCGACCAAGACAGTGGGAGTGA 496
 |||
 Qy 121 G1yG1yAlaPhePheIleLeuGlyLeuGlyGlyPheIleProValaIatPasnLeu 140
 |||
 Db 497 GGTGAGTCTTTTTCATCTTGAAGGCTCTGGGCTTCAATTCCTGTGCTGGAACTT 556
 |||
 Qy 141 HisGlylleLeuArgAbaPheTySerProLeuValProAbaSerMetLysPheGlnIle 160
 |||
 Db 557 CATGGGATCTTACGGGACTTCTACTCACCTGCTGCTGACAGCATGAATTTGAGATT 616
 |||
 Qy 161 G1yG1uAlaLeuTyrlLeuGlylleleSerSer 171
 |||
 Db 617 GGAGAGCTCTTACTGCGGATATTCTTCC 649
 |||
 RESULT 7
 CR628947 652 bp mRNA linear EST 11-AUG-2004
 LOCUS DKEZp469L0623_r1.469 (synonym: pkid1) Pongo pygmaeus cDNA clone
 DKEZp469L0623_5', mRNA sequence.
 ACCESSION CR628947
 VERSION CR628947.1 GI:51125027
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 1 (bases 1 to 652)
 Wambutt, R., Heubner, D., Mewes, H.W., Well, B., Amid, C., Oeanger, A.,
 Fobo, G., Han, M. and Wiemann, S.
 Pongo pygmaeus mRNA (Wambutt, R., Heubner, D., Mewes, H.W., et al.)
 Unpublished (2004)
 TITLE Pongo pygmaeus mRNA (Wambutt, R., Heubner, D., Mewes, H.W., et al.)
 JOURNAL
 COMMENT
 CONTACT: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKF2);
 Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneID=DKEZp469L0623
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
 FEATURES
 source
 location/Qualifiers
 1..652
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKEZp469L0623"
 /issue_type="kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1b="469 (synonym: pkid1)"
 /note="Vector: pSport1_Sfi, Site_1: SfiIA, Site_2: SfiIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.9e-156 Length: 652
 Score: 171.00 Matches: 171
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 74.35% Indels: 0
DB: 7 Gaps: 0
US-09-787-677a-3 (1-230) x CR628947 (1-652)

Qy 1 Meta1aSerLeuGlyLeuGlnLeuValGlyTyr11LeuGlyLeuLeuGlyLeuGly 20
Db 138 ATGGCCCTCTTGCCCTCCCAACTGTGGGCTACATCTTAGGCCCTTCTGGGGCTTTGGGC 197

Qy 21 ThrLeuVal1aMetLeuLeuProSerTTrpLysThrsSerTyrValGly1aSer11e 40
Db 198 ACACTGGTTCCTAGCTGCTCCAGCTGGAACCAAGTTCTTACGTGCGTGCAGCATT 257

Qy 41 ValThr1aValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThsGly 60
Db 258 GTGACAGCAGTGGCTCTTCCAAAGGCTCTGATGAGTGTCACACACAGCAGAGT 317

Qy 61 IleThrGlnCysAap1IleYrSerThrLeuGlyLeuPro1aAap1IleGln1a1a 80
Db 318 ATCAACCAAGTGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGCTGCC 377

Qy 81 Gln1aMetMetVal1ThrSerSerAla1IleSerSerLeu1aCys11e1IleSerVal1 100
Db 378 CAGGCCATGATGATGACATCCAGTCAATCTCTCCCTGGCTGCAATTATCTGTGTG 437

Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArg1aLysAapArgVal1aVal1a 120
Db 438 GGCTAGAGATGACAGCTCTTCTGACAGAAATCCGAGCCAAAGACAGTGCGGTAGCA 497

Qy 121 Gly1aVal1aPhePhe1IleGly1aLeuGly1aPhe1IleProVal1a1aTrpAsnLeu 140
Db 498 GGAGGATCTTTTTCATCTTGGAGGCTCTGGGCTTCACTCTGTGCTGGAATCTT 557

Qy 141 HisGly1IleLeuArgAapPheTyrSerProLeuVal1ProAapSerMetLysPheGlu1Ile 160
Db 558 CATGGGATCTTACCGGACTTCTACTCAACCTGTGCTGACAGCATGAATTTGAGATT 617

Qy 161 Gly1aVal1aLeuTyrLeuGly1a1Ile1SerSer 171
Db 618 GGAGAGGCTCTTTTACTTGGGCAATTATTTCTTCC 650

RESULT 8
LOCUS BG164062 978 bp mRNA linear EST 06-FEB-2001
DEFINITION 602341087F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449212 5',
RNA sequence.
ACCESSION BG164062
VERSION BG164062.1 GI:12670765
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cga@bbs-romail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM10232 row: m column: 21
High quality sequence stop: 689.
Location/Qualifiers
1..978
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

Alignment Scores:
Pred. No.: 1,25e-140 Length: 978
Score: 155.00 Matches: 185
Percent Similarity: 98.93% Conservative: 0
Best Local Similarity: 98.93% Mismatches: 1
Query Match: 67.39% Indels: 2
DB: 4 Gaps: 0
US-09-787-677a-3 (1-230) x BG164062 (1-978)

Qy 1 Meta1aSerLeuGlyLeuGlnLeuValGlyTyr11LeuGlyLeuLeuGlyLeuGly 20
Db 25 ATGGCCCTCTTGCCCTCCCAACTGTGGGCTACATCTTAGGCCCTTCTGGGGCTTTGGGC 83

Qy 21 ThrLeuVal1aMetLeuLeuProSerTTrpLysThrsSerTyrValGly1aSer11e 40
Db 84 ACACTGGTTCCTAGCTGCTCCAGCTGGAACCAAGTTCTTACGTGCGTGCAGCATT 143

Qy 41 ValThr1aValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThsGly 60
Db 144 GTGACAGCAGTGGCTCTTCCAAAGGCTCTGATGAGATGTGCCACACACAGCAGC 203

Qy 61 IleThrGlnCysAap1IleYrSerThrLeuGlyLeuPro1aAap1IleGln1a1a 80
Db 204 ATCAACCAAGTGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGCTGCC 263

Qy 81 Gln1aMetMetVal1ThrSerSerAla1IleSerSerLeu1aCys11e1IleSerVal1 100
Db 264 CAGGCCATGATGATGACATCCAGTCAATCTCTCCCTGGCTGCAATTATCTGTGTG 323

Qy 101 GlyMetArgCysThrValPheCysGlnGluSerArg1aLysAapArgVal1aVal1a 120
Db 324 GGCTAGAGATGACAGCTCTTCTGACAGAAATCCGAGCCAAAGACAGTGCGGTAGCA 383

Qy 121 Gly1aVal1aPhePhe1IleGly1aLeuGly1aPhe1IleProVal1a1aTrpAsnLeu 140
Db 384 GGAGGATCTTTTTCATCTTGGAGGCTCTGGGATTCATCTCTGTGCTGGAATCTT 443

Qy 141 HisGly1IleLeuArgAapPheTyrSerProLeuVal1ProAapSerMetLysPheGlu1Ile 160
Db 444 CATGGGATCTTACCGGACTTCTACTCAACCTGTGCTGACAGCATGAATTTGAGATT 503

Qy 161 Gly1aVal1aLeu-TyrLeuGly1Ile1IleSerSerLeuPheSerLeu1a1aGly1Ile1 180
Db 504 GGAGAGGCTCTTTTACTTGGGCAATTATTTCTCTGTCTCTCCCTGATGCTGGAATCAT 563

Qy 180 eLeuCysPheSerCysSer 186
Db 564 CTTCTGCTTTCTCTGCTCA 582

RESULT 9
LOCUS BG385562 494 bp mRNA linear EST 12-MAR-2001
DEFINITION 602453856F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4582214 5',
RNA sequence.
ACCESSION BG385562
VERSION BG385562.1 GI:13278350
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 494)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNCM304 row: c column: 15
 High quality sequence stop: 493.
 Location/Qualifiers

FEATURES

source

1. 494
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4582214"
 /issue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC_15"
 /note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Alignment Scores:

Pred. No.: 5 52e-139 Length: 494
 Score: 153.00 Matches: 153
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 66.52% Indels: 0
 DB: 4 Gaps: 0

US-09-787-677A-3 (1-230) x BG385562 (1-494)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
 DB 35 ATGGCCTCTCTGGCCCTCAACTGTGGCTACATCTTAGGCTTGGGGCTTTGGGC 94
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLyThrSerSerTrpValGlyAlaSerIle 40
 DB 95 ACACGTGGTTCACATGCTGCTCCCACTGAGAAACAAGTTCTTAATGCGGTGCAGCATT 154
 QY 41 ValThrAlaValGlyPheSerLySGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
 DB 155 GTACAGACATTGGCTTCTCCAAAGGCGCTTCGATGGAATGTGCCACACACAGCAGGC 214
 QY 61 IleThrGlnCysAspIleIleTrpSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 215 ATACACCAAGTGAACATCTAATAGACCCCTTGGCGCTGACATCCAGGCTGCC 274
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 275 CAGGCGCATGATGATGATCAGTCAATCTCCCTCCCTGCGCTGCATTATCTCTGTGTG 334
 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaIleAspAspValAlaValAla 120
 DB 335 GGATGATGATGACAGAGCTTCTGCGCAGAAATCCGAGACCAAGACAGATGGCGGTGCA 394
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaATPAsnLeu 140
 DB 395 GGTGAGATCTTTTTCATCTTGGAGGCGCTCTGGGATTCATCTCTGTGCTGGAAATCTT 454
 QY 141 HisGlyIleLeuArgAspPheTrpSerProLeuValPro 153

DB 455 CATGGATCTCTACGGAGCTTCTACTACACATGCTGCT 493

RESULT 10
 BE513091
 LOCUS
 DEFINITION BE513091 945 bp mRNA linear EST 07-AUG-2000
 601171545F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545171 5',
 mRNA sequence.
 ACCESSION BE513091
 VERSION BE513091.1 GI:9720302
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE 1 (bases 1 to 945)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNCM241 row: 1 column: 12
 High quality sequence start: 36
 High quality sequence stop: 782.
 Location/Qualifiers

FEATURES

source

1. 945
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3545171"
 /issue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC_15"
 /note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Alignment Scores:

Pred. No.: 2.42e-110 Length: 945
 Score: 124.00 Matches: 158
 Percent Similarity: 99.37% Conservative: 0
 Best Local Similarity: 99.37% Mismatches: 1
 Query Match: 53.91% Indels: 1
 DB: 2 Gaps: 0

US-09-787-677A-3 (1-230) x BE513091 (1-945)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
 DB 187 ATGGCCTCTCTGGCCCTCAACTGTGGCTACATCTTAGGCTTGGGGCTTTGGGC 246
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLyThrSerSerTrpValGlyAlaSerIle 40
 DB 247 ACACGTGGTTCACATGCTGCTCCCACTGAGAAACAAGTTCTTAATGCGGTGCAGCATT 306
 QY 41 ValThrAlaValGlyPheSerLySGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
 DB 307 GTACAGACATTGGCTTCTCCAAAGGCGCTTCGATGGAATGTGCCACACACAGCAGGC 366
 QY 61 IleThrGlnCysAspIleIleTrpSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80

Db 367 ATCACCAGTGTGATCATCTATAGACACCTTCTGGGCGCTGACCATCAGGCTGCC 426
 QY 81 GlnAlaMetwetalThrsSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 427 CAGGCCATGATGGATGACATCAGTCAATCTCCCTGGCGCTGATTAATCTGTGTG 486
 QY 101 G1MeArGyGThrValPheCyGInG1uSerArG1a1yAaPArGvAla1aVala1a 120
 Db 487 GGCATGAGATGACAGCTCTCTGCGAGAAATCCGAGCCAAAGACAGTGGCGGTAGCA 546
 QY 121 G1yG1yValPhePheIleLeuG1yG1yLeuLeuG1yPheIleProVala1a1aTPanLeu 140
 Db 547 GGTGAGACTTT-TCATCCTTGGAGGCTCCTGGGATTCATCTCTGTGCTGGAACTT 605
 QY 141 H1G1y11leuArGArPheTyTserProLeuValProAaPserMeTyPheGlu 159
 Db 606 CATGGATCTTACGAGGACTTCTACTCACCAGTGTGCTGACAGCATGAATTTGAA 662

RESULT 11
 LOCUS CR628828 570 bp mRNA linear EST 11-AUG-2004
 DEFINITION DKFZp469B1623_r1 469 (synonym: pk1d1) Pongo pygmaeus cDNA clone
 CR628828
 VERSION CR628828.1 GI:51124908
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus

REFERENCE 1 (bases 1 to 570)
 AUTHORS Ansoorge W., Krieger S., Regiert T., Rittmeller C., Schwager B.,
 Mewes H.W., Well B., Amid C., Osanger A., Fobo G., Han M., and
 Wiemann S.
 Pongo pygmaeus mRNA (Ansoorge W., Krieger S., Regiert T., et al.)
 Unpublished (2004)
 COMMENT MIPS

10101staedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469B1623
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES
 Source
 1..570
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp469B1623"
 /tissue_type="Kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="469 (synonym: pk1d1)"
 /note="Vector: pSPORT1_Sfi; Site_1: SfiIa; Site_2: SfiIb"

ORIGIN

Alignment Scores:
 Pred. No.: 1.3e-108 Length: 570
 Score: 122.00 Matches: 122
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.04% Indels: 0
 DB: 7 Gaps: 0

US-09-787-677a-3 (1-230) x CR628828 (1-570)

QY 1 MetAlaSerLeuG1yLeuGlnLeuValG1yTyrIleLeuG1yLeuLeuG1yLeuLeuG1y 20
 Db 146 ATGGCTCTCTTGGCGCTTCAACTGTGTGGCTATACCTCAGGCTTCTGGGGCTTTTGGGC 205

QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPlyThrsSerSerTyrValG1yAlaSerIle 40
 Db 206 ACATGTTGCCATGCTGCTGCCACACTGGAAAAACAAGTTCTTAACGCGGTGCAGACTT 265
 QY 41 ValThrAlaValG1yPheSerLyG1yLeuTyrMeG1yCysAlaThrIleSerThrGly 60
 Db 266 GTACAGACACTTGGCTTCTCCAAAGGCGCTCTGATGAGAGTGCACACACACAGGT 325
 QY 61 IlleThrGlnCysAaP11eTySerThrLeuLeuG1yLeuProAlaAaP11eGlnAlaAla 80
 Db 326 ATACCCAGTGTACATCTATACACCTTCTTGAGGCTGCCCTGACATCCAGGCTGCC 385
 QY 81 GlnAlaMetwetalThrsSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 386 CAGGCCATGATGGATGACATCAGTCAATCTCCCTGGCGCTGATTAATCTGTGTG 445
 QY 101 G1MeArGyGThrValPheCyGInG1uSerArG1a1yAaPArGvAla1aVala1a 120
 Db 446 GGCATGAGATGACAGCTCTCTGCGAGAAATCCGAGCCAAAGACAGTGGCGGTAGCA 505

RESULT 12
 LOCUS CB999779 758 bp mRNA linear EST 01-MAY-2003
 DEFINITION ABEINCOU13642925 NIH_MGC_186 Homo sapiens cDNA clone
 IMAGE:30322852 5', mRNA sequence.
 CB999779
 VERSION CB999779.1 GI:30294299
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 758)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straubeberg, Ph.D.
 Email: cga@nci.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDCM124 row: 1 column: 05
 High quality sequence stop: 592.

FEATURES
 Source

Location/Qualifiers
 1..758
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30322852"
 /lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_186"
 /note="Organ: Pooled-Skin; Vector: pDNR-Lib; Site_1: SfiI
 (ggccatcgccgc); Site_2: SfiI (ggccgcctggcc); Library is
 oligo-dT primed and directionally cloned. cDNA was
 prepared from a pooled samples of tissues from skin,
 meninges, dura mater, pia mater and choroid plexus. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCATTAATGCTC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGGCGGCGAGCATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 Library"

ORIGIN

Alignment Scores:

Pred. No.:	1,49e-105	Length:	758
Score:	119.00	Matches:	119
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	51.74%	Indels:	0
DB:	6	Gaps:	0

US-09-787-677a-3 (1-230) x CB999779 (1-758)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGlyLeuLeuGly 20
 DB 331 ATGGCCCTCTTGGCTCCCACTTGAGGCTACATCTTAGCCCTTGGGGCTTTGGGC 390
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPlySerSerTyrValGlyAlaSerlle 40
 DB 391 ACACGTGGTCCATGCTGCTCCCACTGGAACAAAGTTCTTATGTCGGTCCAGCATT 450
 QY 41 ValThrAlaValGlyPheSerIyGlyLeuTyrMetGlyCysAlaThrHisSerThGly 60
 DB 451 GTGACAGCAGATTGGCTTCTCAAGGGCTCTGATGGAATGTCACACACAGCAGGC 510
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 511 ATACCCAGGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 570
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 571 CAGGCCATGATGTGATGACATCAGTGCATCTCTCCCTGCGCTGATATCTCTGTG 630
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaVal 119
 DB 631 GGCATGATGATGACAGCTTCTTCTGCGAGGAATCCGAGCAACAGAGTGGCGGTT 687

RESULT 13
 CA389170 459 bp mRNA linear EST 06-NOV-2002
 LOCUS cs06d06.y1 Human Retinal pigment epithelium/choroid cDNA
 DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs06d06
 5', mRNA sequence.

ACCESSION CA389170
 VERSION CA389170.1 GI:24719072
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 459)
 Mistlew,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,
 Touchman,J.W., Bouffard,G., Smith,D., and Peterson,K.
 Expressed sequence tag analysis of human RPE/choroid for the
 NEIBank Project: Over 6000 non-redundant transcripts, novel genes
 and splice variants
 Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL MEDLINE
 PUBLISHED 22103460
 12107410
 COMMENT Contact: Mistlew G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 06 row: d column: 06
 Seq primer: M13RPL reverse primer (ABI).
 Location/Qualifiers

FEATURES
 source
 1..459
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="cs06d06"

ORIGIN

Alignment Scores:

Pred. No.:	6.55e-100	Length:	459
Score:	113.00 <td>Matches:</td> <td>113</td>	Matches:	113
Percent Similarity:	100.00% <td>Conservative:</td> <td>0</td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0</td>	Mismatches:	0
Query Match:	49.13% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	6	Gaps:	0

US-09-787-677a-3 (1-230) x CA389170 (1-459)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGlyLeuLeuGly 20
 DB 121 ATGGCCCTCTTGGCTCCCACTTGAGGCTACATCTTAGCCCTTGGGGCTTTGGGC 180
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPlySerSerTyrValGlyAlaSerlle 40
 DB 181 ACACGTGGTCCATGCTGCTCCCACTGGAACAAAGTTCTTATGTCGGTCCAGCATT 240
 QY 41 ValThrAlaValGlyPheSerIyGlyLeuTyrMetGlyCysAlaThrHisSerThGly 60
 DB 241 GTGACAGCAGATTGGCTTCTCAAGGGCTCTGATGGAATGTCACACACAGCAGGC 300
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 DB 301 ATACCCAGGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 360
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 361 CAGGCCATGATGTGATGACATCAGTGCATCTCTCCCTGCGCTGATATCTCTGTG 420
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAla 113
 DB 421 GGCATGATGATGACAGCTTCTTCTGCGAGGAATCCGAGGC 459

RESULT 14
 CR554772 421 bp mRNA linear EST 12-JUL-2004
 LOCUS DKFZP469E0814.r1.469 (synonym: pkl1) Pongo pygmaeus cDNA clone
 DEFINITION DKFZP469E0814.5', mRNA sequence.

ACCESSION CR554772
 VERSION CR554772.1 GI:50244701
 KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 1 (bases 1 to 421)
 Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
 Oeinger,A., Fobo,G., Han,M., and Wiemann,S.
 Pongo pygmaeus mRNA (Bloeker,H., Boecker,M., Brandt,P., et al.)
 Unpublished (2004)
 Contact: MIPS
 MIPS

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

/tissue_type="RPE/choroid"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="Human Retinal pigment epithelium/choroid cDNA
 (Un-normalized, unamplified): cs"
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
 eyes (75-80 years old) yielded approximately 600 mg of
 dissected RPE/choroid tissue. This in turn yielded 340 ug
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA
 library in the pCMVSPORT6 vector was constructed at Life
 Technologies (Rockville, MD; now part of Invitrogen Corp),
 essentially following the protocols of the SuperScript
 Plasmid System (Invitrogen Corp
 <http://www.invitrogen.com/>). The library code
 designation was cs. For this library, cDNA inserts were
 cloned into the NotI/Mui sites of the vector. EST
 analysis was performed on the unamplified library at the
 NIH Intramural Sequencing Center (NISC)."

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ),
Email: s.wiemann@dkfz-heidelberg.de, sequenced by GBF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany)
within the CDNA sequencing consortium of the German Genome Project.
This clone (DKFZp469E0814) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source

1..421
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp469E0814"
/issue_type="Kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pKid1)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 5.4e-98	421	111	0	0	0	0
Percent Similarity: 100.00%						
Best Local Similarity: 100.00%						
Query Match: 48.26%						

US-09-787-677a-3 (1-230) x CRS54772 (1-421)

Qy 1 MetAlaSerLeuGlyLeuGlnValGlyTyrTleLeuGlyLeuGlyLeuGly 20
Db 89 ATGGCCCTCTCGGCTTCAACCTGTGGGCTACATCCAGCCCTTCTGGGCTTTGGGC 148
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerTle 40
Db 149 ACACTGGTGGCAGTGGCTCCCACTGGGAAACAGATTCTTACGTGGTGGCCAGCATTT 208
Qy 41 ValThrAlaValGlyPheSerTleGlyLeuTrpMetGluCysAlaTrpHisSerThrGly 60
Db 209 GTGACACAGATGGCTTCTCAAGGCTCTCGATGAGTGTGCACACACAGACAGCT 268
Qy 61 TleThrGlnCysAapTleTyrSerThrLeuLeuGlyLeuProAlaAapTleGlnAlaAla 80
Db 269 ATCACCCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCCGTGACATCCAGGCTGCC 328
Qy 81 GlnAlaMetMetValThrSerSerAlaTleSerSerLeuAlaCysTleTleSerValVal 100
Db 329 CAGGCCATGATGAGTGACATCCAGTCAATCTCTCCCTGGGCTGCATTAATCTGTGGTG 388
Qy 101 GlyMetArgCysThrValPheCysGlnGluSer 111
Db 389 GGCATGAGATGCACAGTCTTCTGCCAGGAATCC 421

RESULT 15
AI953481/c 560 bp mRNA linear EST 08-MAR-2000
LOCUS
DEFINITION
AI953481 NCI CGAP Kid1 Homo sapiens CDNA clone IMAGE:2472651 3'
similar to TR:088552 088552 CLAUDIN-2. ;, mRNA sequence.

ACCESSION
AI953481
VERSION
AI953481.1 GI:5745791
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 560)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Issue Procurement: Christopher Moskajuk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.lnl.gov/bdip/image/image.html
Insert Length: 756 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 430.
Location/Qualifiers

FEATURES

source

1..560
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2472651"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid1"
/note="Organ: Kidney; Vector: pTRT3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and as circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 6.86e-97	560	123	0	0	0	0
Percent Similarity: 110.00%						
Best Local Similarity: 99.19%						
Query Match: 47.83%						

US-09-787-677a-3 (1-230) x AI953481 (1-560)

Qy 29 SerTrpLysThrSerSerTyrValGlyAlaSerTleValThrAlaValGlyPheSerTle 48
Db 560 AGCTGAAACAGATTCTTATGTCGGTGGCAGCATTTGTGACAGCATTTGCTTCCAG 501
Qy 49 GlyLeuTrpMetGluCysAlaTrpHisSerThrGlyTleThrGlnCysAapTleTyrSer 68
Db 500 GGCTCTGATGATGTGCACACACACAGCATCAACAGTGTGATCATCTATAGC 441
Qy 69 ThrLeuLeuGlyLeuProAlaAapTleGlnAlaAlaGlnAlaMetMetValThrSerSer 88
Db 440 ACCCTTGGAGGCTGCCCGCTGACATCCAGGCTGCCAGGCSATGATGATGATCCAGT 381
Qy 89 AlaTleSerSerLeuAlaCysTleTleSerValValGlyMetArgCysThrValPheCys 108
Db 380 GCATCTCTCCCTCGGCTGCATTAATCTGTGGTGGGATGAGATGACAGATCTTTTGC 321
Qy 109 GlnGluSerArgAlaValAapTleValAlaValAlaGlyValPhePheTleLeuGly 128
Db 320 CAGGATCTCCGAGCCAAAGACAGATGCGCGTACAGAGTGAAGTCTTTTCACTTGA 261
Qy 129 GlyLeuLeuGly-PheTleProValAlaTyrPheMetLeuGlyTleLeuArgAapPheTle 148
Db 260 GGCTCTTGGATTTATCTCTGTGCTGTGCTGGAATCTTCATGGATCTTACGGACTTTTA 201
Qy 148 rSerProLeu 151
Db 200 CTCACCACTG 191

Tue Dec 21 15:56:19 2004

us-09-787-677a-3.011.rst

Page 11

Search completed: December 20, 2004, 20:21:17
Job time : 3203 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 13:33:26 ; Search time 4299 Seconds

(without alignments)
2530.037 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 1174
Sequence: 1 MASLGQVYVYIGLGLG.....PGQPKVKSRFNSYSLTGYV 230

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2.1/USFTO.spool/US09787677/runat.20122004.132739.19435/app.query.fasta_1.391
-DB=GenEmbl -QFMT=fastaap -SUFFIX=xrge -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdi -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=exc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09787677_QCGN_1.1.3731 @runat.20122004.132739.19435 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_com.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	693	6	CQ732222 Sequence
2	1174	100.0	693	9	AF250558 Homo sapi
3	1174	100.0	1400	6	AR340765 Sequence
4	1174	100.0	1400	6	BD085944 Elongatio

5	1174	100.0	1475	6	AX092348 Sequence
6	1174	100.0	1475	6	AX299996 Sequence
7	1174	100.0	1475	6	AX395213 Sequence
8	1174	100.0	1475	6	AX454606 Sequence
9	1174	100.0	1475	6	AX464358 Sequence
10	1174	100.0	1475	6	AX491084 Sequence
11	1174	100.0	1475	6	AX697065 Sequence
12	1174	100.0	1475	6	AX358474 Homo sapi
13	1174	100.0	1506	9	BC014424 Homo sapi
14	1174	100.0	1618	9	BC071747 Homo sapi
15	1174	100.0	1918	9	AF177340 Homo sapi
16	1174	100.0	2742	6	BD237562 Membrane-
17	1174	100.0	2863	6	AX136129 Sequence
18	1174	100.0	2863	6	BD123517 Secretory
19	1174	100.0	2863	9	AK075371 Homo sapi
20	1174	100.0	2959	9	AK075405 Homo sapi
21	1174	100.0	109465	9	AL158821 Human DNA
22	1170	99.7	1441	6	AX286822 Sequence
23	1162	99.0	633	6	AX497200 Sequence
24	1162	99.0	1524	6	AR340718 Sequence
25	1162	99.0	1524	6	BD085897 Elongatio
26	1119	95.3	953	4	AF358907 Canis fam
27	1114	94.9	1032	4	AB115779 Bos tauru
28	1114	93.6	239385	2	AC109666 Rattus no
29	1099	93.6	250600	2	AC136646 Rattus no
30	1099	93.6	268828	2	AC091513 Rattus no
31	1096	93.4	791	6	AX286824 Sequence
32	1096	93.4	791	6	E31591 E31591 Tigt junct
33	1096	93.4	791	10	AF072128 Mus muscu
34	1096	93.4	2828	10	BC015252 Mus muscu
35	1096	93.4	184872	10	AL572243 BX934932 Gallus ga
36	792.5	67.5	1492	5	AX136475 Sequence
37	581	49.5	615	6	BD123715 Secretory
38	581	49.5	615	6	CQ734026 Sequence
39	571	48.6	720	6	AX134445 Homo sapi
40	571	48.6	720	9	HS4132445 Sequence
41	571	48.6	1174	6	AX376286 Sequence
42	571	48.6	1174	6	AX468678 Sequence
43	571	48.6	1174	6	AX697255 Sequence
44	571	48.6	1174	6	AY358533 Homo sapi
45	571	48.6	1227	9	AY355349 Homo sapi

ALIGNMENTS

RESULT 1
CQ732222
LOCUS CQ732222 693 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 18156 from Patent WO02068579.
ACCESSION CQ732222
VERSION CQ732222.1 GI:42311107
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Rlts, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 18156 06-SEP-2002;

JOURNAL
PE Corporation (NY) (US)
Location/Qualifiers
1. .693
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 9.53e-107 length: 693
Score: 1174.00 Matches: 230

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x CQ732222 (1-693)

```

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 1 ATGGCCCTCTTGCCCACTGATGAGGCTTGGCTTCTGAGGCTTTTGGG 60
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysSerSerTrpValAlaSerIle 40
DB 61 ACACGTGTTCCAGCTGCTGCCAGCTGGAACAAAGTTCTTATGCGGTCCAGCAT 120
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThyGly 60
DB 121 GTGACAGACAGTTGGCTTCTCCAGGCGCTCGATGGAATGTGCCACACAGCAGCAG 180
QY 61 IleThrgIncyAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 181 ATCAACCAGTGTGACATCTATAGCACCCTTCTGGGCTGCCGTGACATCCAGGCTGCC 240
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValIle 100
DB 241 CAGGCCATGATGTGACATCCAGTGCATCTCCCTGCGCTGCATTATCTCTGTGTG 300
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
DB 301 GGCGATGAGATGACAGTCTTCTCCAGGAATCCGACCAAGACAGATGGCGGTAGCA 360
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyLeuGlyPheIleProValAlaTrpAsnLeu 140
DB 361 GGGAGAGCTTTTTCATCTTGGAGGCTCTCGGAGATTCATCTCTGTTGCTGGAACTT 420
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 421 CATGGATTCCTAGGAGCTTCTACTCACTGAGCTGACACAGAAATTTGAGATT 480
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 481 GGAGAGGCTCTTTTACTTGGGCAATATTTCTCCCTGTTCTCCGTATGAGTGCAGATCATC 540
QY 181 LeuCyPheSerCysSerSerGlnArgAspArgSerAntyrTyrAspAlaTyrGlnAla 200
DB 541 CTCGCTTTTCTGCTCATCCAGAGAAATGCTCCAACTAGACAGATGCTTACCAAGCC 600
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValIleSerGlu 220
DB 601 CAACCTCTTGCCACAGAGAGCTCTCCAAAGCTGTGTCACTCCCAAAAGTCAAGAGTGA 660
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 661 TTCAATTCCTACAGCTGACAGGATATGTG 690

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RESULT 2

AF250558 693 bp mRNA linear PRI 10-JUN-2002
 LOCUS Homo sapiens claudin-2 mRNA, complete cds.
 DEFINITION AF250558
 ACCESSION AF250558
 VERSION AF250558.1 GI:9755008
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 693)
 Sakaguchi,T., Gu,X., Golden,H.M., Sub,E., Rhoads,D.B. and
 Reinecker,H.C.
 Cloning of the human claudin-2 5'-flanking region revealed a
 TATA-less promoter with conserved binding sites in mouse and human
 for caudal-related homeodomain proteins and hepatocyte nuclear
 factor-1alpha

JOURNAL J. Biol. Chem. 277 (24), 21361-21370 (2002)
 MEDLINE 22050612
 PUBMED 11934881
 REFERENCE 2 (bases 1 to 693)
 AUTHORS Reinecker,H.-C., Sakaguchi,T. and Golden,H.M.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAR-2000) Gastrointestinal Unit, Massachusetts
 General Hospital, Fruit Street, Boston, MA 02114, USA
 FEATURES
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 GFSKGLMECATSTGTTCDDYSTLLGLPADIOAQMNVTSATISLACISIVGM
 RCTVFOESRAKRVAVAGGVFFILGLGFIIGLVANGLIDLPSPIDSMKEFI
 GEAIVGIISLSPLAGIILCFSSGQNRNSVYDAVQAQPLATSSPPGQPKVK
 SEFNYSISLICY"

ORIGIN

Alignment Scores:

Pred. No.: 9,53e-107 Length: 693
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-787-677A-3 (1-230) x AF250558 (1-693)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
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QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysSerSerTrpValAlaSerIle 40
DB 61 ACACGTGTTCCAGCTGCTGCCAGCTGGAACAAAGTTCTTATGCGGTCCAGCAT 120
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThyGly 60
DB 121 GTGACAGACATTTGGCTTCTCCAGGCGCTCGATGGAATGTGCCACACAGCAGCAG 180
QY 61 IleThrgIncyAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 181 ATCAACCAGTGTGACATCTATAGCACCCTTCTGGGCTGCCGTGACATCCAGGCTGCC 240
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValIle 100
DB 241 CAGGCCATGATGTGACATCCAGTGCATCTCCCTGCGCTGCATTATCTCTGTGTG 300
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
DB 301 GGCGATGAGATGACAGTCTTCTCCAGGAATCCGACCAAGACAGATGGCGGTAGCA 360
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyLeuGlyPheIleProValAlaTrpAsnLeu 140
DB 361 GGGAGAGCTTTTTCATCTTGGAGGCTCTCGGAGATTCATCTCTGTTGCTGGAACTT 420
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 421 CATGGATTCCTAGGAGCTTCTACTCACTGAGCTGACACAGAAATTTGAGATT 480
QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

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Db      481 GAGAGGCTTTTACTTGGGCAATTATTTCTCCCTGTTCCCTGATAGCTGGAATATC 540
Qy      181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntyTyTyAspAlaTyGlnAla 200
Db      541 CTCGCTTTTCCGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 600
Qy      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolyValLysSerGlu 220
Db      601 CAACCTCTTCCCAAGAGAGCTCTCCAAAGGCTGTGCAACCTCCCAAGTCAGAGTGTAG 660
Qy      221 PheAsnSerTySerLeuThrGlyTyTyVal 230
Db      661 TTCAATTCTTACAGCTGACAGGGTATGTG 690

RESULT 3
AR340765      1400 bp      DNA      linear      PAT 17-AUG-2003
LOCUS      Sequence 139 from patent US 6573068.
DEFINITION      AR340765
ACCESSION      AR340765
VERSION      AR340765.1 GI:33732507
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 1400)
AUTHORS      Milne Edwards,V.-B.D., Duclert,A. and Bougueleret,L.
TITLE      Claudin-50 protein
JOURNAL      Patent: US 6573068-A 139 03-JUN-2003;
FEATURES
source      1..1400
              /organism="unknown"
              /mol_type="genomic DNA"

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Alignment Scores:
Pred. No.:      2,24e-106      Length:      1400
Score:      1174.00      Matches:      230
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
              Gaps:      0
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Qy      1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyTrrlleLeuGlyLeuLeuGlyLeuLeuGly 20
Db      36 ATGGCCCTCTTGGGCTTCCCAACTGTGGCTACATCTTAGGCCCTTGGGGCTTTGGGC 95
Qy      21 ThrLeuValAlaMetLeuLeuProSerTrrlyThrSerSerTyTyValGlyAlaSerlle 40
Db      96 ACACGTGGTTCACATGCTGCTCCCACTGAGAAAACAAGTCTTATATGCGGTGCGACGATT 155
Qy      41 ValThrAlaValGlyPheSerLysGlyLeuTrrPwCgLuCyAlaThrHisSerThGly 60
Db      156 GTACACACAGTGGCTTCTCCAAAGGCTCTGTGATGGAATGTGCCACACAGCAGGCGC 215
Qy      61 lletHrGlnCyAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db      216 ATCACCAGGTGACATCTATAGCACCCCTTGTGGGCTGCCCGCTGACATCCAGGCTGCC 275
Qy      81 GlnAlaMetMetValThrSerSerAlaHisSerSerLeuAlaCysIleIleSerValAla 100
Db      276 CAGGCCATGATGTGATCATCAGTGCATCTCCCTCGCTGCGCATTAATCTGTGTGTG 335
Qy      101 GlnMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
Db      336 GGCATGAGATGCACAGCTTCTGCGCAGAAATCCGAGACCAAGACAGAGTGGCGGTAGCA 395
Qy      121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrrPasnLeu 140
Db      396 GGTGGAGTCTTTTTCATCTTGAAGGCTCTGTGGATTCAATCTCTGTGGCTGGAATCTT 455

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Qy      141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGlnIle 160
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Db      516 GAGAGGCTTTTACTTGGGCAATTATTTCTCCCTGTCTCCCTGATAGCTGGAATATC 575
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Db      576 CTCGCTTTTCCGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCC 635
Qy      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolyValLysSerGlu 220
Db      636 CAACCTCTTCCCAAGAGAGCTCTCCAAAGGCTGTGCAACCTCCCAAGTCAGAGTGTAG 695
Qy      221 PheAsnSerTySerLeuThrGlyTyTyVal 230
Db      696 TTCAATTCTTACAGCTGACAGGGTATGTG 725

RESULT 4
BD085944      1400 bp      DNA      linear      PAT 27-AUG-2002
LOCUS      BD085944
DEFINITION      Elongation CDNA of secretory protein.
ACCESSION      BD085944
VERSION      BD085944.1 GI:22631554
KEYWORDS      JP 2001523453-A/86.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 1400)
AUTHORS      Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
TITLE      Elongation CDNA of secretory protein
JOURNAL      Patent: JP 2001523453-A 86 27-NOV-2001;
GENSET
OS      Homo sapiens (human)
PN      JP 2001523453-A/86
PD      27-NOV-2001
PR      13-NOV-1998 JP 2000521191
PR      13-NOV-1997 US 60/066677,17-DEC-1997 US 60/069957 PR
09-FEB-1998 US 60/074121,13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116,04-SEP-1998 US 60/099273 PR LYDIE
BOUGUELERET,AYMERIC DUCLEERT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC      C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,PC
C12N1/21,
PC      C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
Von Heijne matrix
CC      score 5.6399980926514
CC      seq ILGLGLGLTLVA/KL
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Pred. No.:      2,24e-106      Length:      1400
Score:      1174.00      Matches:      230
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
              Gaps:      0
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Db 36 ATGGCCCTCTTGAGCCTCAACTGTGGGGTACATCTCAGGCTTCTGAGGGCTTTGGGC 95
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 Db 96 ACATGGTTCCTCAATGCTGCTCCAGCTGAGAAACAAATTTCTTATGTCGGGGCAGCAT 155
 QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaIleThrHisSerThrGly 60
 Db 156 GTGACACAGATTGGCTCTCCAGGGCTCTGAGTGAATGTCCACACACAGCAGCAGGC 215
 QY 61 IleThrGlnCysAspIleTrpSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 Db 216 ATCACCAGATGTGACATCTATAGACCCCTTCTGGGCTGCGCCGTGACATCAGGCTGCC 275
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 276 CAGGCCATGATGGAGATCAGATCAGATCTCTCCCTGGCTGCAATATCTCTGTGGTG 335
 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaLysAspArgValAlaValAla 120
 Db 336 GGCATGAGATGACAGCTCTTCCAGGATCCGAGCCAGCCAGACAGATGGCGGTAGCA 395
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 Db 396 GGTGAGATCTTTTCATCTCTGAGGCTCTGAGGATTCATCTCTGTCCTGGAACTCT 455
 QY 141 HisGlyIleLeuAlaGlyPheTrpSerProLeuValProAspSerMetLysPheGluIle 160
 Db 456 CATGGGATCTTTCATCTCTGAGGCTCTGAGGATTCATCTCTGTCCTGGAACTCT 515
 QY 161 GlyValAlaLeuTrpLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 516 GAGAGGCTCTTACTGCTGGCATTTCTTCCTGTTCTCCGATGATGCTGAAATCATC 575
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAntyTrpAspAlaTrpGlnAla 200
 Db 576 CTCTGCTTTCTCTCATCTCCAGAAATCGCTCAACTACTAGATGCTTACCAAGCC 635
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
 Db 636 CAACCTCTTCCACAGAGAGCTCTCCAGAGCTGTCAACTCCCAAGCTCAAGAGTAG 695
 QY 221 PheAsnSerTrpSerLeuThrGlyTrpVal 230
 Db 696 TTCATTCTTACAGCTGACAGGATATGTG 725
 RESULT 5
 LOCUS AX092348 1475 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 79 from Patent WO0116318.
 ACCESSION AX092348
 VERSION AX092348.1 GI:13444488
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
 Wood,W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0116318-A 79 08-MAR-2001;
 Genentech, Inc. (US)
 FEATURES
 source location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Alignment Scores:

Pred. No.: 2,38e-106 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
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 Db 182 ACATGGTTCCTCAATGCTGCTCCAGCTGAGAAACAAATTTCTTATGTCGGGGCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaIleThrHisSerThrGly 60
 Db 242 GTGACACAGATTGGCTCTCCAGGGCTCTGAGTGAATGTCCACACACAGCAGCAGGC 301
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 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaLysAspArgValAlaValAla 120
 Db 422 GGTGAGATGTGACAGCTCTTCCAGGATCCGAGATCCGAGCCAGACAGAGTGGCGGTAGCA 481
 QY 121 GlyValValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleTrpAsnLeu 140
 Db 482 GGTGAGATCTTTTCATCTCTGAGGCTCTGAGGATTCATCTCTGTCCTGGAACTCT 541
 QY 141 HisGlyIleLeuAlaGlyPheTrpSerProLeuValProAspSerMetLysPheGluIle 160
 Db 542 CATGGGATCTTTCATCTCTGAGGCTCTGAGGATTCATCTCTGTCCTGGAACTCT 601
 QY 161 GlyValAlaLeuTrpLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GAGAGGCTCTTACTGCTGGCATTTCTTCCTGTTCTCCGATGATGCTGAAATCATC 661
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAntyTrpAspAlaTrpGlnAla 200
 Db 662 CTCTGCTTTCTCTCATCTCCAGAAATCGCTCAACTACTAGATGCTTACCAAGCC 721
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 Db 722 CAACCTCTTCCACAGAGAGCTCTCCAGAGCTGTCAACTCCCAAGCTCAAGAGTAG 781
 QY 221 PheAsnSerTrpSerLeuThrGlyTrpVal 230
 Db 782 TTCATTCTTACAGCTGACAGGATATGTG 811
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 LOCUS AX299996 1475 bp DNA linear PAT 26-NOV-2001
 DEFINITION Sequence 1 from Patent WO0166740.
 ACCESSION AX299996
 VERSION AX299996.1 GI:17129473
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Eaton,D.L., Fong,S., Goddard,A., Godowski,P.J., Grimaldi,C.J.,
 Gurney,A.L., Tuma,D., Watanabe,C.K., Wood,W.I. and Zhang,Z.
 TITLE Compositions and methods for the treatment of immune related
 diseases

JOURNAL Patent: WO 0166740-A 1 13-SEP-2001;
Genentech, Inc. (US)
Location/Qualifiers
1. 1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 2.38e-106 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x AX299996 (1-1475)

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QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
DB 182 ACACGTGGTCCATGCTGCTCCCACTGAGAAACAAAGTTCTTATGCGGTGCAGCAT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 242 GTGACAGCAGATTGGCTTCTCCCAAGGGCTCTGGATGATGTGCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 302 ATCACCAGGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
DB 422 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
QY 121 GlyIleValPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaIleProLeu 140
DB 482 GGTGGAGTCTTTTTCATCTTGGAGGCTCTGGGATTCATCTGCTGGATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGATCTTCTACCACTGGTGGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
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QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAGGCTGGTCAACCTCCCAAGTCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAATTCTACAGCTGACAGGATATGTG 811

RESULT 7
AX395213
LOCUS AX395213 1475 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1 from Patent WO0216429.
ACCESSION AX395213
VERSION AX395213.1 GI:21066244

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Goddard, A., Goddard, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,
Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216429-A 1 28-FEB-2002;
Genentech, Inc. (US)
Location/Qualifiers
1. 1475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 2.38e-106 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x AX395213 (1-1475)

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DB 122 ATGGCCCTCTTGGCTTCACCACTTGAGGCTACATCCTAGGCTTCTGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyrValGlyAlaSerIle 40
DB 182 ACACGTGGTCCATGCTGCTCCCACTGAGAAACAAAGTTCTTATGCGGTGCAGCAT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 242 GTGACAGCAGATTGGCTTCTCCCAAGGGCTCTGGATGATGTGCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
DB 302 ATCACCAGGTGACATCTATAGCACCTTCTGGGCTGCGCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
DB 422 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
QY 121 GlyIleValPhePheIleLeuGlyIleLeuLeuGlyPheIleProValAlaIleProLeu 140
DB 482 GGTGGAGTCTTTTTCATCTTGGAGGCTCTGGGATTCATCTGCTGGATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGATCTTCTACCACTGGTGGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GAGAGAGCTCTTACTTGGGCTTATTTCTTCCCTGTTCTCCGTAGTGGATCATC 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaIleGlnAla 200
DB 662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACATGATGCTTCAAGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAGGCTGGTCAACCTCCCAAGTCAAGAGTGA 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230

Db 782 TTCAATTCCTACAGCCTGACAGGATGTG 811

RESULT 8
AX454606 1475 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 191 from Patent WO0208284.
DEFINITION AX454606
ACCESSION AX454606.1 GI:21713927
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurey, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 191 31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

FEATURES
source 1..1475
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 2,386-106 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-787-677a-3 (1-230) x AX454606 (1-1475)

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QY 21 ThrIleuValAlaMetLeuLeuProSerTrpIlyThrSerSerTrpValGlyAlaSerIle 40
Db 182 ACCTGGTTCCTCAAGCTGCTCCAGCTGAAAACAAGTTCTTATGTCGGGCGCAGCATT 241

QY 41 ValThrAlaValGlyPheSerTrpGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
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QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCC 361

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Db 362 CAGGCCATGATGAGATCCAGATCCAGTATCTCCCTGCGCTCATTTATCTGTGGTG 421

QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaValAspArgValAlaValAla 120
Db 422 GGCATGATGATCAACATCTTCTGCGCAAGATCCGAGCCAAAGACAGATGGCGGTAGCA 481

QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
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QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGATTCCTACAGGACCTTCTACTCACCATCTGCTGCTGACATGAAATTTGAGATT 601

QY 161 GlyAlaAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
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QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCAATTCCTACAGCCTGACAGGATGTG 811

RESULT 9
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LOCUS Sequence 491 from Patent WO0140466.
DEFINITION AX464358
ACCESSION AX464358.1 GI:21899195
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Flisaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0140466-A 491 07-JUN-2001; Genentech Inc. (US)

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/organism="Homo sapiens"
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Alignment Scores:
Pred. No.: 2,386-106 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-787-677a-3 (1-230) x AX464358 (1-1475)

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QY 21 ThrIleuValAlaMetLeuLeuProSerTrpIlyThrSerSerTrpValGlyAlaSerIle 40
Db 182 ACCTGGTTCCTCAAGCTGCTCCAGCTGAAAACAAGTTCTTATGTCGGGCGCAGCATT 241

QY 41 ValThrAlaValGlyPheSerTrpGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGATTGGCTTCTCCAGAGGCTCTGATGGAATGTGCACACACAGACAGGC 301

QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
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QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 362 CAGGCGCATGATGGTATGATCATCCAGTGCATCTCTCCCTGGCTGCATTAATCTCTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIysAspArgValAlaValAla 120
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 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIlePheLeu 140
 DB 482 GGTGAGATCTTTTCACTTCTTGGAGGCTCTCGGATTCATTCCTGTGCTGGAACTT 541
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 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
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 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAAAGCCGTGTCMACTCCCAAAAGTCAAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCATTTCTTACAGCTGACAGGGTATGTG 811

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 LOCUS AX491084
 DEFINITION Sequence 191 from Patent WO0200690.
 ACCESSION AX491084
 VERSION AX491084.1 GI:22323879
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Gurney,A.L., Hillan,K.J., Margera,S.A., Pan,J.,
 Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
 and Ye,W.
 Compositions and methods for the diagnosis and treatment of
 disorders involving angiotensin
 Patent: WO 0200690-A 191 03-JAN-2002;
 Genentech, Inc. (US)

TITLE
 JOURNAL
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 Location/Qualifiers
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 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 2,38e-106 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x AX491084 (1-1475)

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QY 21 ThrLeuValAlaMetLeuLeuProSerTrrPheSerSerTyrValGlyAlaSerIle 40
 DB 182 ACACGTGTGGTGCATGTGTCTCCCACTGAGAAAACAGTTCTTATGTGGTGCACAT 241
 QY 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrrMetGlyCysAlaThrHisSerThrGly 60
 DB 242 GTACACGAGTGGCTTCTTCCAAAGGCTCTGTGATGAAATGTCCACACACAGCAGGC 301
 QY 61 ILeThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 DB 302 ATCACCAGATGATCATATATACACCTTCTGAGGCTGCGCTGCATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
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 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIysAspArgValAlaValAla 120
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 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIlePheLeu 140
 DB 482 GGTGAGATCTTTTCACTTCTTGGAGGCTCTCGGATTCATTCCTGTGCTGGAACTT 541
 QY 141 HisGlyTlleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
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 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 DB 662 CTCTGCTTTTCCGTGCATCCAGAGAAATCGCTCCAACTACTACATGCTTCCAAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAAAGCCGTGTCMACTCCCAAAAGTCAAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCATTTCTTACAGCTGACAGGGTATGTG 811

RESULT 11
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 DEFINITION Sequence 133 from Patent WO0078961.
 ACCESSION AX697065
 VERSION AX697065.1 GI:29498042
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
 Baton,D.L., Gao,W.Q., Pan,J., Botstein,D., Pong,S., Goddard,A.,
 Godowski,P.J., Gurney,A.L., Smith,V., Tamas,D., Wood,W.I.,
 Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
 Secreted and transmembrane polypeptides and nucleic acids encoding
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 Patent: WO 0078961-A 133 28-DEC-2000;
 Genentech Inc. (US)

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 Location/Qualifiers
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 /mol_type="unassigned DNA"
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Alignment Scores:

Pred. No.: 2,38e-106 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677A-3 (1-230) x AY358474 (1-1475)

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 QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaTrpHisSerThrGly 60
 DB 242 GTGACGACATGGCTTCTCCAAAGGCTCTGGATGGAATGTGCCACACACAGCAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
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 QY 101 GlyMetArgCysThrValPheCysGlnGlyLeuSerGlnAlaLysAspArgValAlaValAla 120
 DB 422 GGCATGAGATGACAGCTTCTGTCAGGAATCCGACCCAAAGACAGATGGCGGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
 DB 482 GGTGAGTCTTTTCATCTGTGGAGGCTCTCGGATTCATCTGTGGCTGGAACTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
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 QY 161 GlyGlyAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
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 DB 662 CTCGTCTTTCTGCTCATCCACAGAAATGCTCCAACTACTACGATGCTTACCAAGCC 721
 QY 201 GluProLeuAlaTrpArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
 DB 722 CAACCTCTTGCACAAAGAGCTCTCCAAAGGCTGTGATCACTCCCAAGTCAAGAGTGA 781
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 DB 782 TTCAATTCCTACGCTGACAGGCTAATGTG 811

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 DEFINITION AY358474
 ACCESSION AY358474.1 GI:37182070
 VERSION AY358474.1 GI:37182070
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 1475)
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,B.E.,
 Heldens,S., Huang,A., Kim,H.S., Klimoweki,L., Jin,Y., Johnson,S.,

TITLE
 JOURNAL
 PUBMED
 12975309
 2 (bases 1 to 1475)
 AUTHORS
 Clark,H.F.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (01-JUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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 Pred. No.: 2,38e-106 Length: 1475
 Score: 1174.00 Matches: 230
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 Query Match: 100.00% Indels: 0
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US-09-787-677A-3 (1-230) x AY358474 (1-1475)

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 QY 101 GlyMetArgCysThrValPheCysGlnGlyLeuSerGlnAlaLysAspArgValAlaValAla 120
 DB 422 GGCATGAGATGACAGCTTCTGTCAGGAATCCGACCCAAAGACAGATGGCGGTGCA 481
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Qy	161	GIyGluAlaLeuTyYrLeuGIYlleIleSerSerLeuPheSerLeuIleAlaGIYlleIle	180
Db	602	GGAGAGGCTCTTACTTGGCATTTATTTCTTCCCTGTTCTCCCTGATAGCTGGAAATCATC	661
Qy	181	LeuCySPheSerCySeSerSerGlnaArgaAaHrGSeAaTyTYrAspAlaTyGlnAla	200
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Qy	201	GlnProleuAlaIaHrArgSerSerProArgProGIYleInProPolYVallySerGIu	220
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Qy	221	PheAaSerTYrSerLeuThrGIYTYrAl	230
Db	782	TTCAATCTCTACAGCTCTGACAGGGATATGTG	811
RESULT 13			
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DEFINITION	Homo sapiens claudin 2, mRNA (CDNA clone MGC:20191 IMAGE:4645075), complete cds.		
ACCESSION	BC014424		
VERSION	BC014424.1	GI:15680158	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 1506)		
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Hontela, S.F., Zeeberg, B., Bueltow, K.H., Schaefer, C.F., Bat, N.K., Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Udell, T.B., Topolycki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McEwan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wexler, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huliy, S.W., Vallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shychenko, Y., Bonfield, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Gilmwood, J., Schmitt, J., Myers, R.M., Butcherfield, Y.S., Krzywinski, M.I., Skalka, U., Smalins, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1506)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-rc@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@cgsc.bc.ca		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium LML at: <http://image.lml.gov>
 Series: IRAL.Plate: 29 Row: m Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9966780.

Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.:	2.44e-106	Length:	1506
Score:	1174.00	Matches:	230
Best Local Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-787-677A-3 (1-230) x BC014424 (1-1506)

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Oy      1  MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
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Oy      41  ValThrAlaValGlyPheSerLyGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
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Oy      81  GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db      362 CAGGCCATGATGGTGAATCCAGTCAATGCAATCTCCCTGGCGCTGCATTATCTCTGTGGT 421
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Db 422 GGCATGATGACAGCTCTTCTGCGCAGGAATCCGAGCAAGACAGAGTGGCGGTAGCA 481
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 Qy 141 H1AG11LEULEARGAPHEPHELYRSEPRLEUVALPROAPSERMELTYPHEGLU11E 160
 Db 542 CATGGATCTTACGGAGCTTCTACTCCACTGCTGCTGACAGCATGAATTTGAGATT 601
 Qy 161 G1YGLUALALEUITYLEUGLYLEULESERSERLEUPHESEULEU11EAGLYLE11E 180
 Db 602 GAGAGGCTCTTACTTGAGCATATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATC 661
 Qy 181 LEUCYEPHESERCYSESERSEGINARASARSERSEITYTYRAPPALATYRGINALA 200
 Db 662 CTCTGCTTTTCCGCTCATCCAGAGAAATGCTCCCACTACATGATGCTTACCAAGCC 721
 Qy 201 G1NPROLEUALATFARXSERSEPRORXPROGLYGINPROLYVALLYSERGLU 220
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 Qy 221 PHEASNSERTYRSELEUINRGLYTYRVAL 230
 Db 782 TTCATTCCTACAGCTGACAGGATGTGT 811
 RESULT 14
 BC071747
 LOCUS Homo sapiens claudin 2, mRNA (cDNA clone MGC:88250 IMAGE:30322852), complete cds.
 ACCESSION BC071747
 VERSION BC071747.1 GI:47938251
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1618)
 Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Helel, F., Datchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L., Siepel, M., Soares, M.B., Donald, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ueda, T.B., Tothiyuk, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McGowan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J.J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, J., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 2 (bases 1 to 1618)
 Strauberg, R.
 Direct Submission
 Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokovits
 cDNA Library Preparation: CLOWTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@pdxl.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAL Plate: 57 Row: n Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9966780.
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 Alignment Scores:
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 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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 Db 388 ACACTGTTGCCATGCGTCTCCCACTGGAAGAAACAGTTCTTAGTCGGTGCAGCATT 447
 Qy 41 ValThrAlaValGlyPheSerLgLYLeuTrrPmetGluCyAlaThrHisSerThGly 60
 Db 448 GTGACAGACATGGCTCTCCCAAGGCGCTGATGGAATGTGCACACACAGCAGGC 507
 Qy 61 IleThrGlnCyAspIleTrrSerThrLeuLgLYLeuProAlaAspIleGlnAla 80
 Db 508 ATCACCCAGGTGACATCTTAGACACCTTGGCGCTGCGCCGTGCATCCAGGCTGC 567
 Qy 81 GlnAlaMetMetValTrrSerSerAlaIleSerSerLeuAlaCyAlaIleSerVal 100
 Db 568 CAGGCCATGATGGATCATCATGCAATCTCTCTGCGCTGCATTAATCTCTGCGTG 627
 Qy 101 G1YMetArgCyThrValPheCyGlnGluSerArgAlaIleAspArgValAlaValAla 120

Db 628 GGATGATGATGACAGCTCTTCTCCAGAAATCCGAGCAAGAGAGAGTGGCGGTAGCA 687

Qy 121 GYGLYVALPHEHELLELEUGLYLEULEUGLYPHEHELLEPROVALAATPPAENLEU 140

Db 688 GGTGAGCTCTTTTCACTTCCTTGAGAGGCTCTGGAAATCTTCCTGCTGGAAATCTT 747

Qy 141 HIEGLYILEUARGASPHELYRSEPRLEUVALPROASPSEMETLYSPHEGLIILE 160

Db 748 CATGGATCTTACGGAGCTTCTACTACCACTGGTGGCTTACAGCATGAATTTGAGATT 807

Qy 161 GYGLYVALAULEUYRLEUGLYILELESESERLEUPHESELEULEAGLYILEILE 180

Db 808 GAGAGGCTCTTACTTGGCATTATTCTTCCTGTTTCCCTGATAGCTGGAATATC 867

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Db 868 CTCTGCTTTTCCGCTCATCTCCAGAAATCGCTCCCAACTACTACGATGCTTACCAAGCC 927

Qy 201 GINPROLEUALATHRARGSERSEPRARGPROGLYGINPROLYVALLYSERGLU 220

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RESULT 15

AF177340 1918 bp mRNA linear PRI 03-OCT-2000

LOCUS Homo sapiens clone sp82 claudin 2 mRNA, complete cds.

DEFINITION AF177340

ACCESSION AF177340.1 GI:10503979

VERSION AF177340.1

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1918)

AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.

TITLE Novel human cDNA clone with function of inhibiting cancer cell growth

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1918)

AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.

TITLE Direct Submission

JOURNAL Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai 200032, P.R. China

FEATURES

source location/Qualifiers

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ORIGIN

Alignment Scores: 3.28e-106 Length: 1918

Pred. No.:

Score: 1174.00 Matches: 230

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-787-677a-3 (1-230) x AF177340 (1-1918)

Qy 1 METALSERLEUGLYLEUGINLEUVALGLYTRYILLEUGLYLEULEUGLYLEULEUGLY 20

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Qy 21 THRLEUVALAMETLEUPROSETRPLYSTHSESEYTRYVALGLYALASERILE 40

Db 580 ACACGTGTCACATGCTGCTCCACAGCTGAAAACAGTTCTTATGTCGTGCGCAGCATT 639

Qy 41 VALTHRALVALGLYSESELYSGLYLEUTRPMETGLUCYSAATHRHISSEYRGLY 60

Db 640 GTACAGCAGATTGGCTTCTCCAAAGGCTCTGATGGAATGTCCACACACACAGAGC 699

Qy 61 ILETHRGLNCYASPLIETYSERTHLEULEUGLYLEUPROALASPILLEGINALALA 80

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Db 760 CAGGCGATGATGTGACATCCAGTGCATCTCTCCCTGGCTGCATATCTGTGGTG 819

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Db 820 GGCTATGATGACACATCTTCTCCAGGAATCCCGACCAACACAGATGGCGGTAGCA 879

Qy 121 GYGLYVALPHEHELLELEUGLYLEULEUGLYPHEHELLEPROVALAATPPAENLEU 140

Db 880 GGTGAGCTCTTTTCACTTCCTTGAGAGGCTCTCGGATTCATCTCTGCTGCTGGAATCTT 939

Qy 141 HIEGLYILEUARGASPHELYRSEPRLEUVALPROASPSEMETLYSPHEGLIILE 160

Db 940 CATGGATCTTACGGAGCTTCTACTACCACTGGTGGCTGACAGCATGAATTTGAGATT 999

Qy 161 GYGLYVALAULEUYRLEUGLYILELESESERLEUPHESELEULEAGLYILEILE 180

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Qy 181 LEUCYPHESECYSSERSEGINARGASARGSERASNTYTRYASPALATYRGINALA 200

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Qy 201 GINPROLEUALATHRARGSERSEPRARGPROGLYGINPROLYVALLYSERGLU 220

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Search completed: December 20, 2004, 16:50:19

Job time: 4306 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 13:30:16 ; Search time 497 Seconds
(without alignments)
2429.310 Million cell updates/sec

Title: US-09-787-677A-3
Perfect score: 1174
Sequence: 1 MASLGQLVGYITGLGLG.....PGQPPKXSEFNYSLTGY 230

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	1400	2	AAx97865
2	1174	100.0	1400	10	ADJ45986 Human sec
3	1174	100.0	1400	12	ADP18800 Human sec
4	1174	100.0	1475	3	AAA37060 Human PRO
5	1174	100.0	1475	4	AAFS4296 DNA encod
6	1174	100.0	1475	4	AAAS21489 Human CDN

7	1174	100.0	1475	4	AA515360
8	1174	100.0	1475	4	AA92097
9	1174	100.0	1475	6	AB574417
10	1174	100.0	1475	6	ABL88167
11	1174	100.0	1475	6	ABK11089
12	1174	100.0	1475	6	ABL95656
13	1174	100.0	1475	8	ACA81203
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31	1174	100.0	1475	8	ACA63412
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33	1174	100.0	1475	9	ADA76441
34	1174	100.0	1475	9	ADB17136
35	1174	100.0	1475	9	ADA19091
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37	1174	100.0	1475	9	ADB19499
38	1174	100.0	1475	9	ADB28040
39	1174	100.0	1475	9	ADA86519
40	1174	100.0	1475	9	ADB16083
41	1174	100.0	1475	9	ADA47869
42	1174	100.0	1475	9	ACH03615
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ALIGNMENTS

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AC	AAx97865;
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DT	23-SEP-1999 (first entry)
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DE	Human secreted protein encoding cDNA #53.
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KW	Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;
XX	diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
OS	Homo sapiens.
XX	
PN	W09925825-A2.
XX	
PD	27-MAY-1999.
XX	
PF	13-NOV-1998; 98WO-IB001862.
XX	
PR	13-NOV-1997; 97US-0066677P.
PR	17-DEC-1997; 97US-0069957P.
PR	09-FEB-1998; 98US-0074121P.
PR	13-APR-1998; 98US-0081563P.
PR	10-AUG-1998; 98US-0096116P.
XX	04-SEP-1998; 98US-0099273P.
XX	
PA	(BEST) GENSET.
XX	

PI Bougueleret L, Duclert A, Dumae Milne Edwards J;
 XX WPI; 1999-347472/29.
 DR P-PSDB; AAY36181.
 XX
 PT Extended cDNAs encoding secreted proteins.
 XX
 PS Claim 1; Page 254-255; 307pp; English.
 XX
 CC AAX97813-X97906 represent extended cDNA's which encode novel human
 CC secreted proteins (see AAY36129-Y36222) and which have cytostatic,
 CC thrombotic and osteopathic activity. The extended cDNAs can be used to
 CC express secreted proteins or parts of them or to obtain antibodies
 CC capable of binding to the secreted proteins. They may also be used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC Uses also include design of expression vectors and secretion vectors
 XX
 SQ Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,4e-122	Length:	1400
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-787-677a-3 (1-230) x AAX97865 (1-1400)

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 Db 36 ATGGCCCTCTTGCCCTTCAACTGTGGGCTACATCTCAAGCCCTTGCGGCTTTGGGC 95
 QY 21 ThrIleuValAlaMetLeuLeuProSerTrrIyThrSerSerTyrValGlyAlaSerIle 40
 Db 96 ACCTGCTTCCCACTGCTGCCAGCTCCAGCTGAAACAAATTTCTTATGTCGGTCCAGCAT 155
 QY 41 ValThrAlaValGlyPheSerIyGlyLeuTrpMetGluCysAlaTrpHisSerThGly 60
 Db 156 GTGACAGCAATGGCTTCTCCAGAGGCTCTGAGTGAATGTCCACACACAGCAGCAGGC 215
 QY 61 IleThrGlnCysApeIleTyrSerThrLeuLeuGlyLeuProAlaApeIleGlnAla 80
 Db 216 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCCCTGACATCCAGGCTGCC 275
 QY 81 GlnAlaMetIleValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 276 CAGGCCATGATGGAGACATCCAGCAATCTCTCCCTGGCTTCATTAATCTTGTGTG 335
 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaIyAsaPArGValAlaValAla 120
 Db 336 GGCATGAGATGACACAGCTTCTGCTCCAGGAATCCGAGCCAAAGACAGATGCGGTAGCA 395
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
 Db 396 GGTGAGACTTTTTCATCTTGAGAGGCTCTCTGGAGTTCATCTCTGTTGCTTGAATCTT 455
 QY 141 HisGlyIleLeuArgAapPheTyrSerProLeuValProApeSerMetIyPheGluIle 160
 Db 456 CATGGATCTCAACGGAATCTTACTCACTGATGCTGCTGACAGCAATTTGAAATTT 515
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 516 GAGAGAGCTCTTTCATCTTGAGGATTAATTTCTCTGTTCTCTGATAGCTGGAAATCATC 575
 QY 181 LeuCyApeSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 576 CTCTGCTTTTCTCTGCTCATCCAGAAATGCTCCAACTACTAGATGCTTACCAAGCC 635
 QY 201 GlnProLeuAlaTrpArgSerSerProArgProGlyGlnProPolylValIySerGlu 220
 Db 636 CAACCTCTTGCACAGAGAGCTTCCAAAGGCTGTGATCAACTCCCAAAAGTCAGAGTGA 695

QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 696 TTCAATTCCTACAGCTTGACAGGATATGTC 725

RESULT 2

ADJ45986
 ID ADJ45986 standard; cDNA; 1400 BP.
 XX
 AC ADJ45986;
 XX
 XX
 XX 06-MAY-2004 (first entry)
 DE
 XX

Novel human secreted protein-related cDNA sequence SeqID139.

secreted protein; upstream regulator; gene therapy; protein purification;
 protein synthesis; chromosomal mapping; individual identification;
 forensic; hereditary disease; drug reaction; immunoassay;
 epitope mapping; vaccine; immune system regulation;
 haematopoietic system; tissue growth; reproductive hormone;
 cell migration; blood clotting; receptor/ligand interaction;
 adhesion molecule; assisted drug delivery;
 human glial maturation factor gamma-2; neurite outgrowth;
 neurite resprouting; human; gene; ss.

Homo sapiens.

US2003144490-A1.

31-JUL-2003.

10-DEC-2002; 2002US-00319763.

13-NOV-1997; 97US-0066677P.

17-DEC-1997; 97US-0069957P.

09-FEB-1998; 98US-0074121P.

13-APR-1998; 98US-0081563P.

10-AUG-1998; 98US-0096116P.

04-SEP-1998; 98US-0099273P.

13-NOV-1998; 98US-00191997.

15-SEP-2000; 2000US-00663600.

(EDWA/) EDWARDS J D M.

(DUCL/) DUCLERT A.

(BOUG/) BOUGUELERET L.

PI Edwards JDM, Duclert A, Bougueleret L;

DR WPI; 2003-851788/79.

XX P-PSDB; ADJ46033.

PT New nucleic acid encoding secreted human polypeptides, useful e.g. in
 PT gene therapy or diagnosis, also encoded proteins, potential therapeutic
 PT agents.

PS Claim 3; SEQ ID NO 139; 269pp; English.

XX This invention relates to novel purified isolated polynucleotides which
 XX comprise a sequence that encodes at least 10 amino acids (aa) from any of
 XX 48 secreted polypeptide sequences, given in the specification, or
 XX fragments of polypeptides encoded by human cDNA contained in the
 XX corresponding deposited clone. The DNA sequences of the invention encode
 XX secreted proteins (or their fragments) and can be used to
 XX identify/isolate upstream regulators, potentially useful in gene therapy
 XX or protein purification, by controlling protein synthesis, as probes for
 XX chromosomal mapping, identification of individuals, and for diagnosis or
 XX forensic, for example identifying genes associated with hereditary
 XX diseases or drug reactions, for recombinant expression of the encoded
 XX proteins or where the DNA sequence encodes a signal peptide, for
 XX directing secretion of heterologous polypeptides. Polypeptides encoded by
 XX the DNA sequences of the invention can be used to raise antibodies,
 XX useful for detecting the polypeptide, as (ant)agonists, or for preparing
 XX anti-idiotypic antibodies, as tags in for example immunoassays, epitope
 XX mapping or vaccines, also as molecular weight markers, to screen for

CC agents with biological activity and as therapeutic agents with.
CC potentially, a very wide range of activities, for example regulation of
CC the immune or haematopoietic systems, tissue growth, reproductive
CC hormones, cell migration, blood clotting or receptor/ligand interaction,
CC also as adhesion molecules for assisted drug delivery. A typical isolated
CC sequence is human glial maturation factor gamma-2, which stimulates
CC neurite outgrowth and resprouting. The present sequence is a cDNA
CC sequence which encodes a human secreted protein of the invention.

XX Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,4e-122	Length:	1400
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-787-677a-3 (1-230) x ADP18800 (1-1400)

```
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
Db 36 ATGGCCCTCTTGGCTCCAACTGTGGGTACATCCTAGGCTTCTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerTyrValGlyAlaSerIle 40
Db 96 ACACGTGGTCCATGCTGCTCCAGCTGGAACAAAGTTCTATATGCGGTGCCACGATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 156 GTACACGACATTTGGCTTCTCAAGGCTCTGATGAAATGTGCAACACAGCACAGGC 215
QY 61 IleThrGlnCysAspIleYrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 216 ATCACCAGGTGATCATCTATAGACACCTTCTGGGCTGCCGCTGATCCAGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 276 CAGGCGCATGATGATGACATCAGTGAATCTCCCTGCGCTGCATTAATCTCTGTGGT 335
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleValAspArgValAlaValAla 120
Db 336 GGCATGATGATGACAGCTTCTGCGAGAAATCCGACCCAAAGACAGATGGCGGTGCA 395
QY 121 GlyIleValPhePheIleLeuGlyLeuLeuGlyPheIleProValAlaIleProVal 140
Db 396 GGTGGATCTTTTTCATCTTGGAGGCTCTGCGGATTCATTCCTGTTGCTGGAATCTT 455
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 160
Db 456 CATGGGATCTTACGGGACCTTCTACCACTGGTGTGCTCAAGCATGAATTTGAAATT 515
QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 516 GAGAGAGCTTTTACTTGGGATTAATTTCTCCCTGTTCCCGATGAGCTGGAAATATC 575
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 576 CTCTGCTTTTCCGCTCATCCAGAAATCGCTCCAACTACTACATGATGCTCAAGCC 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db 636 CAACCTCTTGCCCAAGAGACTCTCCAAAGGCTGTGCAACTCCCAAAAGTCAAGAGTAG 695
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 696 TTCAATTCTTACAGCTGACAGGATATG 725
```

RESULT 3
ADP18800
ID ADP18800 standard; cDNA; 1400 BP.
XX

AC ADP18800;
XX 26-AUG-2004 (first entry)
XX Human secreted polynucleotide #56.
XX Human secreted polynucleotide #56.
XX Homo sapiens.
XX US2004110939-A1.
XX 10-JUN-2004.
XX 15-OCT-2001; 2001US-00978360.
XX 17-DEC-1998; 98WO-IB002122.
XX 09-FEB-1999; 99WO-IB000282.
XX 21-JUN-2000; 2000WO-IB000951.
XX 15-SEP-2000; 2000US-0063600.
XX (BEST) GENSET SA.
XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;
XX Duclert A;
XX WPI, 2004-440404/41.
XX P-PSDB; ADP19205.
XX New isolated polynucleotide encoding secreted polypeptide, useful for
XX gene therapy, or in diagnostic procedures to identify individuals having
XX genetic diseases resulting from abnormal expression of the genes.
XX Claim 1; SEQ ID NO 56; 113pp; English.
XX The invention relates to human cDNA sequences that encode human secreted
XX proteins. The invention also relates to an antibody that specifically
XX binds to a polypeptide of the invention and a method of binding the
XX polypeptide to an antibody. The polynucleotides are useful for expressing
XX the entire secreted proteins which they encode and for distinguishing
XX human tissues and cells from non-human tissues and cells, and for
XX distinguishing between human tissues and cells that do or do not express
XX the polynucleotides comprising the cDNAs. The polynucleotides and
XX polypeptides are useful in forensic procedures or diagnostic procedures
XX to identify individuals with genetic diseases resulting from abnormal
XX expression of the genes corresponding to the cDNAs. The sequences are
XX also useful in gene therapy to control or treat genetic diseases. This
XX sequence represents a human secreted polynucleotide of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html.

XX Sequence 1400 BP; 326 A; 392 C; 346 G; 336 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1,4e-122	Length:	1400
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

XX US-09-787-677a-3 (1-230) x ADP18800 (1-1400)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
Db 36 ATGGCCCTCTTGGCTCCAACTGTGGGTACATCCTAGGCTTCTGGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerTyrValGlyAlaSerIle 40
Db 96 ACACGTGGTCCATGCTGCTCCAGCTGGAACAAAGTTCTATATGCGGTGCCACGATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
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Db 156 GTGACGACATTGGCTTCTCCAGAGGCTCTGGATGATGATGTCACACACAGCAGCGC 215
Qy 61 IIEThrGlnCysAspIIEYrSerThrLeuGlnGlyLeuProAlaApIIIEGlnAla 80
Db 216 ATCACCAGTGTGACATCTATAGCACCTTCTGGGCTGCGCCGTGACATCCAGCTGCC 275
Qy 81 GAlaAlaMetMetValIThrSerSerAlaIIIESerSerLeuAlaCysIIIEIIESerVal 100
Db 276 CAGGCCATGATGGTGACATCCAGTGCATCTCTCCCTGGCTGCTGATTCCTCTGTGTG 335
Qy 101 G1YMeArGcYsThrValIhneCyEgInG1uSerArGAlaIuYsAsPArGValAlaValAla 120
Db 336 GGCATGAGATGCAAGCTCTTGTCCAGAAATCCGAGCAAGACAGATGCGCTGCA 395
Qy 121 G1YGIYValPhePheIIIEleuG1YLeuGlnGlyPheIIIEProValAlaITrPAnLeu 140
Db 396 GGtGAGTCTTTTTCATCTTGGAGGCTCCTGGGATTCATCTCTGTGCTGGATCTT 455
Qy 141 H1EG1YIIEleuArGAPhETySerProleuValIProArSerMetIYsPheG1uIIE 160
Db 456 CATGGATCTTACCGGACTTCTACTACACACTGTGCTGACAGCATGAAATTTGAGATT 515
Qy 161 G1YGIuAlaLeuYrLeuG1YIIEIIESerSerLeuPheSerIIEuIIEAlaG1YIIE 180
Db 516 GAGAGGCTCTTACTTGGGATATTCTTCCCTGTTCTCCGATAGCTGATCATC 575
Qy 181 LeuCyAPheSerCySserSerGlnArGAsArSerAntYrYAsPAlaITrGlnAla 200
Db 576 CTCTGCTTTCTCTCTCATCCAGAAATGCTCAACTGATGATGCTTACCAAGCC 635
Qy 201 G1nProleuAlaIThrArGSerSerProArGProG1nProPArValIIESerG1u 220
Db 636 CAACCTCTTGCAAGAGCTCTCCAGAGCTGTCACACTGCCATGCCAAGTCAAGTGA 695
Qy 221 PheAnSerTYrSerLeuThrG1YrVal 230
Db 696 TTCAATTCCTACAGCTGACAGGATGTG 725

RESULT 4
AAA37060
ID AAA37060 standard; cDNA, 1475 BP.
XX
AC AAA37060;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1356 (UNQ705) cDNA sequence SEQ ID NO:133.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 03-SEP-1998; 98US-0099536P.
PR 03-SEP-1998; 98US-0099566P.
PR 03-SEP-1998; 98US-0099598P.
PR 03-SEP-1998; 98US-0099602P.
PR 03-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
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PR 17-SEP-1998; 98US-0100710P.
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PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
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PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
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PR 23-SEP-1998; 98US-0101475P.
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PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
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PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 30-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 30-SEP-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103499P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103936P.
PR 07-OCT-1998; 98US-0103967P.
PR 08-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105002P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105149P.
PR 22-OCT-1998; 98US-0105263P.
PR 26-OCT-1998; 98US-0105683P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
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PR 27-OCT-1998; 98US-0105882P.
 PR 27-OCT-1998; 98US-0106062P.
 PR 28-OCT-1998; 98US-0106023P.
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 PR 28-OCT-1998; 98US-0106178P.
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 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106456P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 DR WPI; 2000-237871/20.
 DR P-PSDB; AAY99378.

XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX
 PS Claim 2; Fig 77; 773pp; English.

XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-787-677A-3 (1-230) x AAA37060 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20

DB 122 ATGGCTCTCTTGGCTCCACCTTGCGGCTGACATCTAGGCTTGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
 DB 182 ACACGTGTTCCTCAGTGTGCTCCACGTGGAAACAAAGTTCTTATGCGGTGCAGCATT 241
 QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
 DB 242 GTACACGACGATTGGCTTCCCAAGGGCTCTGGATGGAATGTCCACACACACACAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 DB 302 ATCACCAGTGTGACATCTATACACCTTCTTGAGGCTGCCCTGCATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 DB 362 CAGGCCATGATGTGTGACATCCAGTGCATCTCTCCCTGGCTGCATTTATCTGTGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
 DB 422 GGCATGAGATGCACAGTCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGGTAGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrPheLeu 140
 DB 482 GGTGGAGCTTTTTCATCTTGGAGGCTCTCTGGATTCATCTCTGTGCTTGGAACTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 542 CATGGATCTTACGGGACCTTCTACACCATGCTGCTGCAGCATGAATTTGAGATT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 602 GGAGAGGCTCTTACCTTGGCATTTATTTCTTCCCTGTCTCCCTGATGATGCATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAspTyrTyrAspAlaTyrGlnAla 200
 DB 662 CTCTGCTTTTCTCTGCTCATCCAGAAATGCTTCAACTACTACATGCTTCCAAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 DB 722 CACCTCTTGCCCAAGGAGCTCTCCAGGCTGTGCACTCTCCAAAGTCAAGAGTAGAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCATTTCTTACAGCTGACAGGATGTG 811

RESULT 5

ID AAF54296 standard; DNA; 1475 BP.

XX AAF54296;

AC 02-APR-2001 (first entry)

DE DNA encoding protein of the invention #39.

KW Secreted; transmembrane; gene therapy; ss.

OS Unidentified.

PN WO200078961-A1.

PD 28-DEC-2000.

PF 18-FEB-2000; 2000MC-US004342.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-014758P.

XX 26-JUL-1999; 99US-0145698P.

XX 01-SEP-1999; 99MO-US020111.

XX 29-OCT-1999; 99US-0162506P.

XX 30-NOV-1999; 99MO-US028313.

PR 02-DEC-1999; 99MO-US028551.
PR 16-DEC-1999; 99MO-US030095.
PR 05-JAN-2000; 2000MO-US000219.
PR 06-JAN-2000; 2000MO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI;
XX
DR WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Claim 2; Fig 77; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1 51e-122 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-787-677a-3 (1-230) x AAF54296 (1-1475)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 122 ATGGCCCTCTTGGCCTCAACCTGTGGGCTACATCTCAGGCTTGTGGGCTTTGGGC 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrTrpThrSerSerTyrValAlaSerIle 40
Db 182 ACACTGGTTCACAGCTGCTCCAGCTGGAACCAAGTTCTTATGTCGGGCGCAGCATT 241
QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTrpMetGluCysAlaThrAlaSerThrGly 60
Db 242 GTGACACAGCTTGGCTTCTCCAGGGCTCTGAGATGGAATGTCACACACAGCAGCGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db 302 ATGACCCAGCTGATCATCTATAGCACCTTCTGGGCTGCGCGCTGACATCAGGCTGCC 361
QY 81 GlnAlaMetLeuValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGGAGATCCAGTGCATCTCTCCCTCGGCTCATTTATCTCTGGGTG 421
QY 101 GlnMetArgCysThrValPheCysGlnGluSerAlaValAspArgValAlaValAla 120
Db 422 GGCATGAGATGACAGCTTCTTCCAGGAATCCGAGCCAAAGACAGAGTGGCGGTGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGAGATCTTTTCATCTTGAAGGCTCTCTGGGATTCATCTCGTTGCTGGAATCTT 541
QY 141 HisGlyIleLeuAlaGAspPheTyrSerProLeuValProAspSerMetValPheGluIle 160
Db 542 CATGGGATCTCCACGAGCTTCTACTCACTGCTGGTGCACACATGAAATTTGAGATT 601
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

Db 602 GGAGAGCTCTTACTTGGGCAATTATTTCTCCCTGTCTCCCTGATAGCTGAATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnAlaGAsnArgSerAsnTyrTrpAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCCCTGCATCTCCAGAGAAATGCTCCAACTACTACATGCTCTTCCAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValIleSerGlu 220
Db 722 CAACCTTCTCCACAGAGCTCTCCAGGCTGTCTCACTCCCAAGTCAGAGTGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATTCCTACAGCTGACAGGATATGTG 811
RESULT 6
AAS21489
ID AAS21489 standard; cDNA; 1475 BP.
XX
AC AAS21489;
XX
AC 24-OCT-2001 (first entry)
XX
DT Human cDNA sequence encoding for PRO1356 polypeptide.
XX
DE Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor- α ; TNF- α ; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy; ss.
XX
XX Homo sapiens.
OS
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000MO-US032678.
XX
PR 01-DEC-1999; 99MO-US028301.
PR 01-DEC-1999; 99MO-US028634.
PR 02-DEC-1999; 99MO-US028551.
PR 02-DEC-1999; 99MO-US028564.
PR 02-DEC-1999; 99MO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99MO-US030095.
PR 20-DEC-1999; 99MO-US030911.
PR 20-DEC-1999; 99MO-US030999.
PR 30-DEC-1999; 99MO-US031274.
PR 30-DEC-1999; 99MO-US031243.
PR 05-JAN-2000; 2000MO-US000219.
PR 06-JAN-2000; 2000MO-US000277.
PR 06-JAN-2000; 2000MO-US000376.
PR 11-FEB-2000; 2000MO-US003565.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US004814.
PR 24-FEB-2000; 2000MO-US005004.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000MO-US006319.
PR 15-MAR-2000; 2000MO-US006884.
PR 20-MAR-2000; 2000MO-US007377.
PR 21-MAR-2000; 2000MO-US007532.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014841.
PR 02-JUN-2000; 2000MO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000MO-US020710.
PR 11-AUG-2000; 2000MO-US022031.

PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023528.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WP1; 2001-408281/43.
 P-PSDB; AAU21417.
 XX
 DR Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 3; Fig 491; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes, or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-787-677A-3 (1-230) x AAS21489 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
 Db 122 ATGGCCCTCTTGGCTCCCAACTGTGGCTGACATCTCTAGCCCTTCGGGGCTTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACGTGGTCCATGCTGCTCCCACTGAGAAACAAAGTTCTTATGCGGTCCAGCAATT 241
 QY 41 ValThrAlaValAlaGlyPheSerLeuGlyLeuTyrPheGlyCysAlaThrHisSerThrGly 60
 Db 242 GTGACAGCAGATGGCTTCTCCCAAGGGCTCTGATGAGAAATGTGCACACACAGCAGAGC 301
 QY 61 IleThrGlnGlyAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 302 ATCACCAGAGTACACATTAAGACCTTCTGGGCTGCGCGGTGACATCCAGGCTGCC 361
 QY 81 GluAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 362 CAGGCCATGATGGTGAATCCAGTGCATATCTCTCTGCGCTGCAATTATCTGTGGTG 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
 Db 422 GGCATGAGATGACAGACTCTTCTGCGAGGAATCCGAGCCAAAGCAGAGTGGCGGTAGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 482 GGTGAGCTCTTTTCATCTTGAGGCTCTGAGATTCATCTGTGGCTGGAAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 Db 542 CATGGATCCTTAGCGGACTTCTACTACCACTGGTGCTGACAGCATGAATTTGAATT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 602 GGAAGGCTCTTACTTGGGCAATTAATTTCTCTGTTCCCTCGATAGCTGGAAATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAntTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTGCTCTTTCCTGCTCATCCAGAGAAATGCTCCAACTACTACATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 Db 722 CAACCTCTTCCCAAGAGACTCTCCAGGCTGTGTAACCTCCAAAGTCAAGAGTGAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGGATATGTG 811
 RESULT 7
 AAS15360
 ID AAS15360 standard; cDNA; 1475 BP.
 XX
 AC AAS15360;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE cDNA encoding human PRO1356 polypeptide.
 XX
 KW Human; PRO1356; clone DNA64886-1601; immune-related disorder;
 KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
 KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
 KW neoplasia; transplantation associated disease; gene therapy;
 KW immunosuppressive; anti-inflammatory; antidiabetic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..814
 FT /*tag= a
 FT /product= "PRO1356 polypeptide"
 FT /*tag= b
 FT mat_peptide 194..811
 FT /*tag= c
 PN WO200166740-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001MO-US006666.
 XX
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191015P.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 24-AUG-2000; 2000MO-US023528.
 PR 01-DEC-2000; 2000MO-US032678.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL,
 PI Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WP1: 2001-625876/72.
 DR P-PSDB; AAU09178.
 XX Nucleic acids encoding PRO polypeptides, useful for detecting and
 PT treating immune related diseases and disorders in mammals including
 PT autoimmune diseases, inflammatory diseases and asthma.
 XX Claim 2; Fig 1; 122pp; English.
 XX The present invention relates to the isolation of 9 novel human PRO
 CC polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.
 CC The novel PRO polypeptides include PRO1356, PRO1884, PRO3444,
 CC PRO3151, PRO4322, PRO9964, PRO10008 and PRO19598. The cDNA sequences
 CC encoding these PRO polypeptides have been designated as clones DNA64886-
 CC 1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273, DNA82223-2567,
 CC DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g.
 CC vaccines) containing PRO polypeptides and methods of using these
 CC compositions are useful in the treatment and diagnosis of immune-related
 CC disorders. Such disorders include immune-mediated inflammatory disorders
 CC (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.
 CC diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),
 CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.
 CC rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),
 CC demyelinating diseases of the peripheral or central nervous system (e.g.
 CC Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact
 CC dermatitis), neoplasias and transplantation associated diseases. The
 CC polynucleotide sequences of the invention may be used in gene therapy.
 CC AAU15360-AAU15368 represent cDNA sequences encoding for the novel human
 CC PRO polypeptides of the invention
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-787-677A-3 (1-230) x AAU15360 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 122 ATGGCCCTCTTGAGCCCTCCAACTTGAGCTACATCTTAGGCTTCTGGGACCTTTGGGC 181
 QY 21 ThrIleuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACGTGTTGGCAGTGTGCTCCAGCTGGAAACAAAGTTCTTATGTCGGGCCAGCATTT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaIleThrIleSerThrGly 60
 Db 242 GTGACACAGTGTGCTTCTCCAAAGGCTCTGAGATGTGCACACACAGCAGCAGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlyAla 80
 Db 302 ATCACCCAGTGTGACATCTATAGCACCTTGTGGGCTTGGCCGCTGACATCAGGCTGCC 361
 QY 81 GlnAlaMetMetValIleThrSerSerAlaIleSerSerIleuAlaCysIleIleSerValAl 100
 Db 362 CAGGCCATGATGTGACATCAGTGCAGTGCATCTCCCTGGGCTGCATATCTCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaValAspArgValAlaValAla 120
 Db 422 GGCATGTGAGTGCACAGTCTTCTGCCAGAAATCCGAGCCAAAGACAGTGGCGTAGCA 481
 QY 121 GlyValValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 482 GGTGGAGTCTTTTTCATCTTGGAGGCTCTGGGATTCATCTCTGTGGCTGGAAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLeuPheGluIle 160

Db 542 CATGGATCTTACGGGACCTTCTACTACACACAGTGTGCTGCAGCATGAATTTGAGATT 601
 QY 161 GlyGlnAlaLeuTyrIleLeuSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GGAGAGGCTTTTACTTGGGCAATTATTTCTTCTGTTCTCCGTGATAGCTGGATATCTC 661
 QY 181 LeuCysePheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCGCTTTCTTCGCTCATCTCCAGAGAAATCGCTCCAACTACATGCTCCAAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValIleSerGlu 220
 Db 722 CAACCTTCTCCCAAGAGACCTCTCCAAAGGCTGTGTCACCTCCAAAGTCAAGAGTAG 781
 QY 221 PheAsnSerTyrSerLeuTyrGlyTyrVal 230
 Db 782 TTCATTTCTTACAGGCTGCAGAGGGATGTG 811
 RESULT 8
 ID AAF92097 standard; cDNA; 1475 BP.
 XX AAF92097;
 AC AAF92097;
 DT 15-MAY-2001 (first entry)
 XX Human PRO1356 cDNA.
 DE Human PRO1356 cDNA.
 XX Human; PRO protein; mapping; ss.
 KW Homo sapiens.
 OS Homo sapiens.
 XX WO200116318-A2.
 XX 08-MAR-2001.
 PD 24-AUG-2000; 2000MO-US023328.
 XX 01-SEP-1999; 99MO-US020111.
 PR 15-SEP-1999; 99MO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000MO-US014642.
 PR 05-JUN-2000; 2000US-0209832P.
 PA (GERTH) GENENTECH INC.
 XX Earon DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX WP1: 2001-183260/18.
 DR P-PSDB; AAB87565.
 XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 XX Claim 2; Fig 79; 278pp; English.
 XX The present sequence is the coding sequence for a human PRO polypeptide
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
 CC antagonists or anti-PRO antibodies are useful for preparation of a
 CC medicament useful in the treatment of a condition which is responsive to
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,51e-122	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-787-677a-3 (1-230) x AAF92097 (1-1475)

```
QY      1 MetAlSerLeuGInLeuValGlyTyrIleuGlyLeuLeuGlyLeuLeuGly 20
        |||
DB      122 ATGGCCTCTTGGCTCCAACTTGCGCTACATCTTAGGCTTCTGGGGCTTTGGGC 181
        |||
QY      21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
        |||
DB      182 ACACTGCTGCCATGCTGCTCCCAAGTGAACAAAGTTCTTATGCGGTGCAGCATT 241
        |||
QY      41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
        |||
DB      242 GTGACGACGATGGCTGCTTCCCAAGGCGCTCTGATGGAATGCCACACACACAGCGC 301
        |||
QY      61 IleThrGlyCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
        |||
DB      302 ATCAACCAAGTACATCTTAGACACCTTCTGGGCTGCGCGTACATCCAGGCTGCC 361
        |||
QY      81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
        |||
DB      362 CAGGCGCATGATGGTGCATCATCAGTGCATCTCCCTCGGCGCATATTCTCGTGGTG 421
        |||
QY      101 GlyMetArgCysThrValPheCysGlnGlnSerThrAlaAlaAspArgValAlaValAla 120
        |||
DB      422 GGCATAGAGATGACAGCTCTTCCCAAGGATCCCGAGCCCAAGACAGAGTGGCGTAGCA 481
        |||
QY      121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
        |||
DB      482 GGTGGAGCTCTTTTCACTTCTTGAGAGCTCTCTGGGATTCATCTCTGCTGGAACTCT 541
        |||
QY      141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
        |||
DB      542 CATGGATCTCTACGGGACTTCTACTCACCACTGGTGCACAGCAGCAAGAAATTGAGATT 601
        |||
QY      161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
        |||
DB      602 GGAAGAGCTCTTACCTGGGCAATTATTTCTTCCCTGTTCTCCCTGATGAGTGAATCATC 661
        |||
QY      181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTrpTyrAspAlaTyrGlnAla 200
        |||
DB      662 CTCTGCTTTTCCGCTCATCTCCAGAGAAATGCTCCCACTACACGATGCTTCCCAAGCC 721
        |||
QY      201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
        |||
DB      722 CAACCTCTTGCCCAAGAGAGCTCTCCAGGCGCTGGTAACTCTCCAAAGCAAGAGAGAG 781
        |||
QY      221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
        |||
DB      782 TTCAAATTCCTACAGCTGACAGGATATGTG 811
        |||
```

RESULT 9

ABST74417 standard; cDNA; 1475 BP.

XX ABST74417;

XX 10-DEC-2002 (first entry)

DE Human cDNA encoding secreted/transmembrane protein PRO3356.

XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

XX US2002119130-A1.

XX 29-AUG-2002.

XX 06-DEC-2001; 2001US-00006867.

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XX      29-OCT-1997; 97US-0063435P.
XX      29-OCT-1997; 97US-0064215P.
XX      22-APR-1998; 98US-0082797P.
XX      29-APR-1998; 98US-0083495P.
XX      15-MAY-1998; 98US-0085579P.
XX      02-JUN-1998; 98US-0087759P.
XX      04-JUN-1998; 98US-0088021P.
XX      04-JUN-1998; 98US-0088029P.
XX      04-JUN-1998; 98US-0088030P.
XX      10-JUN-1998; 98US-0088734P.
XX      10-JUN-1998; 98US-0088740P.
XX      10-JUN-1998; 98US-0088811P.
XX      10-JUN-1998; 98US-0088824P.
XX      10-JUN-1998; 98US-0088825P.
XX      11-JUN-1998; 98US-0088863P.
XX      12-JUN-1998; 98US-0089105P.
XX      16-JUN-1998; 98US-0089514P.
XX      17-JUN-1998; 98US-0089553P.
XX      19-JUN-1998; 98US-0089952P.
XX      22-JUN-1998; 98US-0090246P.
XX      24-JUN-1998; 98US-0090444P.
XX      25-JUN-1998; 98US-0090688P.
XX      25-JUN-1998; 98US-0090696P.
XX      26-JUN-1998; 98US-0090862P.
XX      02-JUL-1998; 98US-0091628P.
XX      10-AUG-1998; 98US-0096012P.
XX      17-AUG-1998; 98US-0096757P.
XX      18-AUG-1998; 98US-0096949P.
XX      18-AUG-1998; 98US-0096959P.
XX      26-AUG-1998; 98US-0097954P.
XX      26-AUG-1998; 98US-0097971P.
XX      26-AUG-1998; 98US-0097979P.
XX      01-SEP-1998; 98US-0098749P.
XX      10-SEP-1998; 98US-0099741P.
XX      10-SEP-1998; 98US-0099763P.
XX      10-SEP-1998; 98US-0099792P.
XX      10-SEP-1998; 98US-0099812P.
XX      10-SEP-1998; 98US-0099815P.
XX      16-SEP-1998; 98US-0100627P.
XX      16-SEP-1998; 98US-0100627P.
XX      16-SEP-1998; 98US-0100662P.
XX      16-SEP-1998; 98US-0100662P.
XX      17-SEP-1998; 98US-0100683P.
XX      17-SEP-1998; 98US-0100684P.
XX      17-SEP-1998; 98US-0100930P.
XX      17-SEP-1998; 98US-0101279P.
XX      22-SEP-1998; 98US-0101379P.
XX      23-SEP-1998; 98US-0101475P.
XX      24-SEP-1998; 98US-0101738P.
XX      24-SEP-1998; 98US-0101743P.
XX      24-SEP-1998; 98US-0101916P.
XX      30-SEP-1998; 98US-0102570P.
XX      06-OCT-1998; 98US-0103449P.
XX      08-MAR-1999; 99US-00505028.
XX      14-MAY-1999; 99US-00510733.
XX      02-JUN-1999; 99US-00512252.
XX      01-SEP-1999; 99US-00520111.
XX      15-SEP-1999; 99US-00521090.
XX      15-SEP-1999; 99US-00521194.
XX      22-DEC-1999; 99US-005030720.
XX      18-FEB-2000; 2000US-00504341.
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PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 01-DEC-2000; 2000MO-US032378.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 01-MAR-2001; 2001MO-US006666.
 PR 30-MAY-2001; 2001MO-US017443.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 PI Batton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI, Godowski PJ;
 XX WPI: 2002-731348/79.
 DR P-PSDB; ABG95890.
 PT
 PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 XX
 PS Claim 2; Fig 79; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, C/G, H or I or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the

CC invention
 XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 1,51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conserved: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-787-677A-3 (1-230) X ABS74417 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
 Db 122 ATGGCCCTCTTGCCCTCCCAAGCTGGGGCTTAACCTTAGGCTTCGGGGCTTTGGGC 181
 QY 21 ThrIleuValAlaMetLeuLeuProSerTyrIleThrSerTyrValGlyAlaSerIle 40
 Db 182 ACAGTGTTCGATGCTGCTGCTCCAGCTGGAAACAAAGTCTTAGTGGGTGCAGCATT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
 Db 242 GTGACAGACAGTGGCTTCTCCAAAGGGCTCTGGATGGAAATGGCACACACAGCAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
 Db 302 ATCCACCGATGTACATCTATACACCTTCTGGCTGCTGCTGATCCAGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAl 100
 Db 362 CAGGCCATGATGTGATGACATCATGCAATCTCTCTGCTGCTGATCTCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnIleSerArgAlaIleAspArgValAlaValAla 120
 Db 422 GGATGATGATGACAGCTTCTGCGCAGGAATCCGACCAAGACAGAGTGGCGGTGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIlePheLeu 140
 Db 482 GGTGGACCTCTTTCATCTTGAGGGCTCTGGATTCATTCCTGTGGCTGGAAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
 Db 542 CATGGATCTTACGGGACTTCTTCACTCACTGCTGCTGACAGCAAGAAATTTGAATT 601
 QY 161 GlyGlnAlaLeuTyrIleGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 Db 602 GGAAGGCTCTTACTTGGGCAATTAATTCCTGTTCTCCGATGAGCTGGAAATCATC 661
 QY 181 LeuCyAPheSerCysSerSerGlnArgAsnArgSerAntTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCGCTCTTTCCTGCTATCCAGAGAAATCGCTCCAACTACATGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPheValIleSerGlu 220
 Db 722 CAACCTTTGGCCACAGAGACTCTCCAGGCTGGTCAACTCCCAAGTCAAGAGTACG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGGGTATGTG 811
 RESULT 10
 ABL88167
 ID ABL88167 standard; cDNA; 1475 BP.
 XX ABL88167;
 AC
 DT 16-MAY-2002 (first entry)
 XX
 XX Human PRO1356 cDNA sequence SEQ ID NO:191.
 DE
 XX Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;

KM vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiotensin disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping; gene; ss.

OS Homo sapiens.

XX W0200200690-A2.

XX 03-JAN-2002.

PD 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 22-JAN-2001; 2001WO-US034956.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006656.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00806889.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 30-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF,

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,

XX WPI; 2002-090516/12.

XX P-PSDB; ABB84912.

PS Claim 2; Fig 191; 565pp; English.

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABB88259 to ABB88267 represent primers and probes used in the
 CC exemplification of the present invention

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,51e-122	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-787-677a-3 (1-230) x ABL88167 (1-1475)

Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20

Db 122 ATGGCCCTCTTGGCCCTCCAACTTGGGCTTACATCTTACGCTTGGGGCTTTGGGC 181

Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40

Db 182 ACACTGGTTCACATGCTGCTCCAGCTGAGAAACAAGTCTTATGCGGTGCAGCATT 241

Qy 41 ValThrAlaValGlyPheSerLeuGlyLeuTyrMetGlyCysValAlaThrIleSerThyGly 60

Db 242 GTACACAGACTGCTTCTCCAAAGGCTCTGATGGAATGTGCACACACAGCAGGC 301

Qy 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80

Db 302 ATCACCAGGTGATCATCTATACACCTCTTGGGCTGCGCTGACATCCAGGCTGCC 361

Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100

Db 362 CAGGCCATGATGTGTGATCATCAGTGCATCTCTCTGCGCTGCATTTATCTGTGGTG 421

Qy 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaIleAspArgValAlaValAla 120

Db 422 GGCATGATGATGACAGCTTCTTCCAGGAATCCGAGCCAAACAGAGTGGGATGCA 481

Qy 121 GlyIleValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIlePheLeu 140

Db 482 GGTGAGCTCTTTTCATCTTGAAGGCTCTGGATTCATCTCTGCTGGATCTT 541

Qy 141 HisGlyIleLeuAlaArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 160

Db 542 CATGGATCTTACGGGACTTCTACTCACCACTGGTGCACAGCATGAATTTAGATTT 601

Qy 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180

Db 602 GGAAGGCTCTTATCTTGGCATTTATTTCTCTCTCTCTGATGAGTGAATATC 661

Qy 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAspTyrTyrAspAlaTyrGlnAla 200

Db 662 CTCTGCTTTCTTCTGCTCATCTCCAGAGAAATCGCTCCAACTACATGAGCTTACAGCC 721

Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220

Db 722 CAACCTCTTCCCAAGAGAGCTCTCCAGGCTGTGTCACCTCCAAAGTCAAGAGTGAG 781

Qy 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230

Db 782 TTCATTTCTTACAGCCTGACAGGATGATG 811

RESULT 11

ABK11089 standard; cDNA; 1475 BP.

XX

AC ABK11089;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE CDNA encoding tumour-associated antigenic target protein, TAT134.
 XX
 KM TAT134; Tumour-associated Antigenic Target; tumour; breast cancer;
 KM colorectal cancer; lung cancer; liver cancer; ovarian cancer;
 KM central nervous system cancer; bladder cancer; melanoma;
 KM pancreatic cancer; leukaemia; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..814
 FT /*tag= a
 FT /product= "TAT134"
 FT /note= "Tumour-associated antigenic target"
 XX
 PN WC200216429-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-JUN-2001; 2001WO-US020118.
 XX
 PR 26-SEP-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US023451P.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,
 PI Wood WI, Wu TD, Zhang Z;
 XX
 DR MPI; 2002-280917/32.
 DR P-PSDB; AAU76534.
 XX
 PT Novel isolated tumor-associated antigenic target polypeptides which are
 PT useful as targets for cancer therapy and diagnosis in mammals.
 XX
 PS Claim 1; Fig 1; 121pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigenic target
 CC polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the
 CC polynucleotides (II) encoding them. (II) is useful for diagnosing the
 CC presence of a tumour in a mammal, where the level of expression of (II)
 CC is indicative on the presence of tumour in the mammal from which the test
 CC sample was obtained. Antibody to (I) is useful for killing a cancer cell,
 CC (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,
 CC an ovarian cancer cell, a central nervous system (CNS) cancer cell, a
 CC melanoma cell, a bladder cancer cell, a pancreatic cancer cell, a
 CC melanoma cell or a leukaemia cell) that expresses (I). Oligonucleotides
 CC hybridising to (II) are useful as diagnostic probes, antisense
 CC oligonucleotide probes or for encoding fragments of full length TAT
 CC polypeptide. (II) is also useful in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA probes, for constructing
 CC hybridisation probes for mapping the gene encoding TAT and for genetic
 CC analysis of individuals with genetic disorders. (II) is also useful for
 CC generating either transgenic animals or knockout animals, and in gene
 CC therapy. The TAT polypeptides and nucleic acids may also be used for
 CC tissue typing and the TAT polypeptides are useful for screening compounds
 CC that mimic the TAT polypeptide (agonist) or prevent the effect of TAT
 CC polypeptide (antagonist). The antibody is useful for staging TAT
 CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT
 CC polypeptide from cells, for detection and quantitation of TAT polypeptide
 CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
 CC Western blot. The antibodies are also useful for treating a TAT-
 CC expressing cancer or alleviating one or more symptoms of cancer in a
 CC mammal. The present sequence represents the coding sequence of TAT134
 XX
 XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1 51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-787-677a-3 (1-230) x ABK11089 (1-1475)
 QY 1 MeaLaseRLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
 DB 122 ATGGCCTCTTGGCCCTCAACTGTGGCTACATCTAGGCCCTTGGGGCTTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerThrIleThrSerSerTyrValAlaSerIle 40
 DB 182 ACCTGGTTCCTAGCTGCTCCAGCTGGAACAAAGTTCTTATGTCGGTCCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
 DB 242 GTGACAGCACTTGGCTTCTCCAGGGCTCTGGATGGAATGTGCCACACAGCAGGCC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 DB 302 ATCACCCAGTGTGACATCTATAGACCCCTCTGGGCTGCGCTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 DB 362 CAGGCCATGATGGGATCAGATCAGGCAATCTCTCCCTGGCTGTCATTAATCTCTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
 DB 422 GGCATGATGCACAGCTTCTTCCAGGATCCGAGCAACAAAGAGTGGGTGCA 481
 QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPheLeu 140
 DB 482 GGTGAGCTTTTTCATCTTGGAGGCTCTGGGATTCATTCCTGTGCTGGAAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProIlePheMetIlePheGlu 160
 DB 542 CATGGATCTTACCGGACTTCTACTCCACTGTGTCTTACAGCATGAATTTGAAT 601
 QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 DB 602 GGAGAGCTCTTACTTGGCATTAATTTCTTCTTCCGATAGCTGGAAATCATC 661
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAntTyrTyrAspAlaTyrGlnAla 200
 DB 662 CTGTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACATCGATGCTTACCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyIleProIleValIleSerGlu 220
 DB 722 CAACTTTCGCCAAGAGCTCTCCAAAGCTGTCAACCTCCCAAGTCAAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 782 TTCAATTCCTACAGCTCGACAGGTATGTG 811
 RESULT 12
 ABL95656 standard; cDNA; 1475 BP.
 ID ABL95656
 AC ABL95656;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 XX Human angiogenesis related cDNA PRO1356 SEQ ID NO: 191.
 DE Human; angiogenesis; PEO protein; cardiovascularisation; wound; cancer;
 KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KM cardiatic; cyostatic; antiangiogenic; hypotensive; vulnary;
 KM antiarteriosclerotic; gene; ss.

XX Homo sapiens.
 OS
 XX
 XX WO200208284-A2.
 XX
 XX
 PD 31-JAN-2002.
 XX
 XX 09-JUL-2001; 2001WO-US021735.
 XX
 XX 20-JUL-2000; 2000US-0219556P.
 XX 25-JUL-2000; 2000US-0220624P.
 XX 25-JUL-2000; 2000US-0220664P.
 XX 28-JUL-2000; 2000WO-US020710.
 XX 02-AUG-2000; 2000US-0222658P.
 XX 17-AUG-2000; 2000US-00643657.
 XX 23-AUG-2000; 2000WO-US023522.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 07-SEP-2000; 2000US-0230978P.
 XX 18-SEP-2000; 2000US-00664610.
 XX 18-SEP-2000; 2000US-00665350.
 XX 24-OCT-2000; 2000US-0242922P.
 XX 08-NOV-2000; 2000US-00709238.
 XX 08-NOV-2000; 2000WO-US030952.
 XX 10-NOV-2000; 2000WO-US030873.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000US-00747259.
 XX 20-DEC-2000; 2000WO-US034956.
 XX 22-JAN-2001; 2001US-00767609.
 XX 28-FEB-2001; 2001US-00796498.
 XX 28-FEB-2001; 2001WO-US006520.
 XX 01-MAR-2001; 2001WO-US006666.
 XX 09-MAR-2001; 2001US-00802706.
 XX 14-MAR-2001; 2001US-00808899.
 XX 22-MAR-2001; 2001US-00816744.
 XX 05-APR-2001; 2001US-00828366.
 XX 10-MAY-2001; 2001US-00854208.
 XX 10-MAY-2001; 2001US-00854280.
 XX 25-MAY-2001; 2001US-00866028.
 XX 25-MAY-2001; 2001US-00865034.
 XX 25-MAY-2001; 2001WO-US017092.
 XX 30-MAY-2001; 2001US-00870574.
 XX 30-MAY-2001; 2001WO-US017443.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 20-JUN-2001; 2001WO-US019692.
 XX
 XX (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 XX MPI: 2002-171999/22.
 XX P-PSDB; ABB95518.
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 XX PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 XX PT infarction), endothelial or angiogenic disorders in a mammal.

PS Claim 1; Fig 191; 567bp; English.
 XX
 XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention
 XX
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-787-677A-3 (1-230) x ABB95656 (1-1475)
 QY 1 MetAlaSerLeuGlyLeuGluValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 122 ATGGCCCTCTTGGCCCTCCCACTTGAGGCTACATCCCTTCTGGGGCTTGGGC 181
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrThrSerSerTyrValGlyAlaSerIle 40
 Db 182 ACACGTGTGCCATGCTGCTGCCACCTGGAATAACAGTTCTTAGTCGGTGACAGATT 241
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
 Db 242 GTACACAGAGTTGGCTTCTCCCAAGGGCCCTTGATGAATGCCACACACACAGCGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrIleLeuGlyLeuProAlaAspIleGlnAla 80
 Db 302 ATCACCAGGTGATACATCTATACACCTTCTGGGCTGCGCGTGCATCCAGCGTCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 Db 362 CAGGCCATGATGTGTGACATCCAGTGCATCTCCCTGGCCGATTAATCTGTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAla 120
 Db 422 GGCATGAGATGACACAGCTTCTCCCGAGATCCCGACAAAGACAGAGTGGGTAGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrPantLeu 140
 Db 482 GGTGAGATCTTTCATCTTGAGAGCCCTCTGGATTCATCTCTGTGCTGGAACTTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 Db 542 CATGGATCTCTACGGGACTTCTACTACACCATGCTGTCAGCATGAATTTGGAGTT 601
 QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 602 GGAGAGGCTCTTACTTGGGCAATTATTTCTCCCTGTTCCCTGATAGTGAATCATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 Db 662 CTCTGCTTTTCCGCTCATCTCCAGAAATCGCTCAACTACATGATGCTTCAAGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIleValLysSerGlu 220
 Db 722 CAACCTCTGCCCAAGAGAGCTCTCCAAAGCCCTGGTCAACCTCCCAAGTCAAGAGTAG 781
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGGTATGTG 811
 RESULT 13
 ACA91203

ID ACA91203 standard; cDNA; 1475 BP.
 XX ACA91203;
 AC 11-JUL-2003 (first entry)
 DT 11-JUL-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO1356 cDNA.
 DE
 XX Human; secreted and transmembrane protein; PRO; antibody therapy;
 KM pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
 OS Homo sapiens.
 XX US2003018173-A1.
 PN 23-JAN-2003.
 XX 01-MAY-2002; 2002US-00063515.
 PF 06-DEC-2001; 2001US-0006867.
 XX (GETH) GENENTECH INC.
 PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 PI WPI; 2003-401702/38.
 DR P-PSDB; AB090915.
 XX New antibody useful for identifying PRO polypeptides, for affinity
 PT purification of PRO polypeptides, and for preparing a medicament for
 PT diagnosing or treating conditions responsive to the antibody or PRO
 PT polypeptide.
 XX Disclosure; Fig 79; 345pp; English.
 XX The invention describes an antibody that specifically binds to a PRO
 CC polypeptide having a fully defined amino acid sequence given in the
 CC specification. The antibody is useful in identifying PRO polypeptides
 CC useful for various industrial applications, including pharmaceuticals,
 CC diagnostics, biosensors and bioreactors. The antibody is also used for
 CC affinity purification of PRO polypeptides from recombinant cell culture
 CC or natural sources. The antibody, PRO polypeptide, or its agonists or
 CC antagonists, may be used for preparing a medicament for diagnosing or
 CC treating a condition responsive to the antibody, PRO polypeptide, or its
 CC agonists or antagonists. This sequence encodes a novel human secreted and
 CC transmembrane PRO polypeptide
 CC
 XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No: 1.51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservaive: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0
 US-09-787-677a-3 (1-230) x ACA91203 (1-1475)
 QY 1 MetAlaSerLeuGIyLeuGlnLeuValGIyTyrIleLeuGIyLeuLeuGIyLeuLeuGIy 20
 Db 122 ATGGCCCTCTTGGCCCTTCAACTGTGGGCTACATCCAGCCCTTTCGGGCTTTGGGC 181
 QY 21 ThrIleuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGIyAlaSerIle 40
 Db 182 ACACTGGTTCGACATGCTCTCCAGCTGGAACCAAGTTCTTAGTCGTCGACGACATT 241
 QY 41 ValThrIleValGIyPheSerLeuGIyLeuTyrMetGIyCysValIleThrIleSerThGIy 60
 Db 242 GTGACACAGAGTTGGCTTCTCCAAAGGGCTTGGATGGATGTGCACACAGACAGAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGIyLeuProAlaAspIleGlnAla 80

Db 302 ATCACCAGGTGACATCTATAGACACCTTCTGGGCTGCCCGCTACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 362 CAGGCCATGATGGTGTGACATTCAGTGCATCTCTCCCTGGCTGACATATCTCTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaValAla 120
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 QY 121 GlyGIyValIlePhePheIleLeuGIyGIyLeuLeuGIyPheIleProValAlaTyrPheLeu 140
 Db 482 GGTGAGTCTTTTCACTCTTGAGGCTCTGGGATTCATTCCTGTCCTGCAATCTT 541
 QY 141 HisGIyIleLeuAlaArgAspPheTyrSerProLeuValProAspSerMetIlePheGluIle 160
 Db 542 CATGGATCCTTACGGGACTTCTACTACACCTGTGTGACAGCATGAATTTGAGATT 601
 QY 161 GlyGlnAlaLeuTyrLeuGIyIleIleSerSerLeuPheSerLeuIleAlaGIyIleIle 180
 Db 602 GGAAGGCTCTTACCTTGGGCAATTTCTCCCTGTCCTGATAGCTGATATC 661
 QY 181 LeuCysePheSerCysSerSerGlnArgAsnArgSerAsnTyrTrpAlaTyrGlnAla 200
 Db 662 CTCGCTTTCTGCTCATCTCCAGAAATCGCTCCACTACATGATGCTCAAGGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGIyGlnProProIleValIleSerGlu 220
 Db 722 CAACCTTTTCCCAAGAGACTCTCCAAAGGCTGTGTCAACCTCCAAAGTCAAGATGAG 781
 QY 221 PheAsnSerTyrSerLeuThrGIyTyrVal 230
 Db 782 TTCAATTCCTACAGCTGACAGGATATGTG 811
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 ACD81580
 ID ACD81580 standard; cDNA; 1475 BP.
 XX
 AC ACD81580;
 XX 18-SEP-2003 (first entry)
 DT
 XX Human cDNA encoding secreted/transmembrane protein PRO1356.
 DE
 XX Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
 KM cytosolic.
 OS Homo sapiens.
 XX US2003009013-A1.
 PN 09-JAN-2003.
 XX 01-MAY-2002; 2002US-00063519.
 PF 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99KO-US005028.
 PR 14-MAY-1999; 99US-0031832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000KO-US004341.
 PR 01-MAR-2000; 2000KO-US0050501.
 PR 02-MAR-2000; 2000KO-US005841.
 PR 21-MAR-2000; 2000KO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000MO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000MO-US034956.
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 PR 28-FEB-2001; 2001MO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00006867.
 PA (GETH) GENENTECH INC.
 XX Eston DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-447384/42.
 DR P-PSDB; ABO33974.
 XX
 PT New isolated antibody specifically binding a PRO polypeptide, useful for
 PT the preparation of a medicament for treating disorders with the aberrant
 PT expression or activity of the PRO polypeptide, such as tumor conditions
 PT and cancer.
 PS Disclosure; Fig 79; 223pp; English.
 XX
 CC The invention relates to an antibody that binds to a secreted or
 CC transmembrane protein designated PRO1446 appearing as ABO33941. The
 CC protein is one of 84 PRO polypeptides which (along with their encoding
 CC nucleic acids) are disclosed in the specification. The methods and
 CC compositions of the present invention are useful for the preparation of a
 CC medicament for the treatment of disorders associated with the aberrant
 CC expression or activity of the PRO polypeptide, such as tumor conditions
 CC and cancer. They can also be used to generate transgenic or knockout
 CC animals useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
 CC molecular weight markers for protein electrophoresis, chromosome
 CC identification and tissue typing. The antibodies may be used in various
 CC diagnostic, competitive binding and/or immunoprecipitation assays. The
 CC present sequence encodes a PRO polypeptide
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.51e-122 Length: 1475
 Score: 1174.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 QY 21 ThrLeuValAlaMetLeuLeuProSerTTrpLysThrSerSerTyrValGlyAlaSerIle 40
 DB 182 ACATGCTGCTCCATGCTGCTCCACGCTGAAACAGATTCTTATGTCGGGCGCAGCAT 241
 QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaTrpHisSerThrGly 60

DB 242 GTGACAGCAGTTGGCTTCTCCAGAGGCGCTTGATGGAATGTGCCACACACAGCAGGC 301
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaIleGlnAla 80
 DB 302 ATCACCAGGTGATCATCTATACACCTTCTGGGCTGCGCCGCTGACATCCAGGCTGCC 361
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 DB 362 CAGGCCATGATGATGATGATCATTCAGTGCATATCTCTCCCTGCGCTGATATCTCTGGTG 421
 QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaIleAspArgValAlaValAla 120
 DB 422 GGCATGATGATGATGATGATCTTCTCCAGGAATCCGAGCCAAACAGAGTGGCGATGCA 481
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
 DB 482 GGTGAGTCTTTTCACTCTTGAGAGGCTCTCGGATTCATCTCTGTGCTGGAATCTT 541
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
 DB 542 CATGGATCTCTAGGAGCTTCTACTCACCCTGTGCTGACAGCATGAATTTGAGATT 601
 QY 161 GlyAlaAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 DB 602 GAGAGGCTCTTACTTGGCATATTTCTTCTCTGCTGATAGCTGATATC 661
 QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTrpAlaTyrGlnAla 200
 DB 662 CTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTAGATGCTCCAGGCC 721
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 DB 722 CAACCTTGTGCCCAAGAGAGCTCTCCAGGCTGTGTCACCTCCCAAGTCAAGAGTGA 781
 QY 221 PheAsnSerTyrSerLeuTrpGlyTyrVal 230
 DB 782 TTCAATTCTTACAGCTTGAAGGATATGTG 811
 RESULT 15
 ID ACA60402 standard; cDNA; 1475 BP.
 AC ACA60402;
 XX 11-JUN-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO1356 cDNA.
 XX Human; secreted and transmembrane polypeptide; gene;
 KW ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;
 KW therapeutic agent screening; chromosome identification; tissue typing;
 KW gene therapy.
 XX Homo sapiens.
 OS US2003018183-A1.
 PN 23-JAN-2003.
 PD 01-MAY-2002; 2002US-00063512.
 PF 06-DEC-2001; 2001US-0006867.
 PR (GETH) GENENTECH INC.
 XX Eston DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-330984/31.
 DR P-PSDB; ABU71991.
 XX
 PT New secreted and transmembrane PRO polypeptides and nucleic acid
 PT molecules encoding the polypeptides, useful in gene therapy or preparing

PT a medicament for treating a condition that is responsive to the PRO
polypeptide or antibody.

PS Disclosure; Fig 79; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide

XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-51e-122	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-787-677A-3 (1-230) x ACA60402 (1-1475)

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QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
Db 182 ACACTGGTGGCAGTCGCTCCAGCGAACAAGTTCTTATGTCGGTCAGCATT 241
QY 41 ValThrAlaValGlyPheSerTyrGlyLeuTrpMetGluCysAlaTrpHisSerThrGly 60
Db 242 GTGACAGACAGTGGCTTCTCAAGGCTCTGGAATGCAATGCCACACAGCAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProIleAspIleGlnAla 80
Db 302 ATCAACCAGTGTGACATCTATAGCACCTTCTGGGCTGCCGCTGACATCCAGGCTGCC 361
QY 81 GluAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
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QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATGAGATCCACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGATGCCGTAGCA 481
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Db 482 GGTGAGCTTTTTCATCTTGAGGCTCTCTGGAGATTCCTGTTGCTGGAACTCTT 541
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QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 602 GAGAGAGCTCTTTTACTGGGCATTATTTCTTCTCTCTGATGCTGGAATCATC 661
QY 181 LeuCybPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 662 CTCTGCTTTTCTCTCTCTCTCCAGGAAATCGTCCAACTACTAGATGCTTACCAAGCC 721
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QY 201 GluProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db 722 CAACCTCTTCCACAGGAGCTCTCCAGGCTGTGTCACCTCCAAAGTCAGAGTGAAG 761
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QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 782 TTCATTCTTACAGCTGACAGGGTATGTG 811
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Search completed: December 20, 2004, 14:45:07
Job time : 504 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 14:29:01 ; Search time 93 Seconds
(without alignments)
1757.865 Million cell updates/sec

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Perfect score: 1174
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :

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6: /cgnt 6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1174	100.0	1475	US-10-140-002-491	Sequence 491, App
3	1162	99.0	1524	US-09-663-600A-45	Sequence 45, App
4	442.5	37.7	1655	US-09-300-958A-22	Sequence 22, App
5	442.5	37.7	1705	US-09-205-258-106	Sequence 106, App
6	437	37.2	708	US-09-620-312D-986	Sequence 986, App
7	430	36.6	1253	US-09-673-395A-71	Sequence 71, App
8	422	35.9	1554	US-09-895-652A-14	Sequence 14, App
9	407.5	34.7	3443	US-09-886-683A-3	Sequence 3, App
10	407.5	34.7	3483	US-09-130-491-3	Sequence 3, App
11	380	32.4	1722	US-09-489-847-93	Sequence 93, App
12	334	28.4	1380	US-09-489-847-125	Sequence 125, App

13	314.5	26.8	1155	4	US-09-603-552-2	Sequence 2, App
14	275	23.4	1353	3	US-09-724-864-32	Sequence 32, App
15	232	19.8	363	2	US-08-966-316-8	Sequence 8, App
16	229	19.5	413	3	US-09-188-930-55	Sequence 55, App
17	229	19.5	413	4	US-09-312-283C-55	Sequence 55, App
18	225.5	19.2	615	4	US-09-621-976-1835	Sequence 1835, App
19	221	18.8	441	4	US-09-404-879A-104	Sequence 104, App
20	221	18.8	441	4	US-09-338-933-104	Sequence 104, App
21	221	18.8	441	4	US-09-215-681-104	Sequence 104, App
22	221	18.8	441	4	US-09-216-003A-104	Sequence 104, App
23	221	18.8	441	4	US-09-667-857-104	Sequence 104, App
24	198	16.9	427	4	US-09-603-552-8	Sequence 8, App
25	185.5	15.8	1801	1	US-08-557-917A-1	Sequence 1, App
26	185.5	15.8	1801	3	US-09-084-153-1	Sequence 1, App
27	185.5	15.8	1801	3	US-09-084-079-1	Sequence 1, App
28	179	15.2	2243	3	US-09-084-079-1	Sequence 1, App
29	174.5	14.9	413	4	US-09-621-976-360	Sequence 360, App
30	161.5	13.8	541	4	US-09-603-552-7	Sequence 7, App
31	159.5	13.6	514	4	US-09-919-039-70	Sequence 70, App
32	131	11.2	253	4	US-09-603-552-6	Sequence 6, App
33	126	10.7	208	4	US-09-603-552-10	Sequence 10, App
34	124.5	10.6	316	4	US-09-702-705-976	Sequence 976, App
35	124.5	10.6	316	4	US-09-736-457-976	Sequence 976, App
36	124.5	10.6	316	4	US-09-614-124B-976	Sequence 976, App
37	124.5	10.6	316	4	US-09-671-325-976	Sequence 976, App
38	124.5	10.6	316	4	US-09-658-824-976	Sequence 976, App
39	119.5	10.2	1558	3	US-09-123-030-7	Sequence 7, App
40	106.5	9.1	350	4	US-09-621-976-13474	Sequence 13474, App
41	100	8.5	1332	4	US-09-489-039A-995	Sequence 995, App
42	99	8.4	840	4	US-09-252-991A-14392	Sequence 14392, App
43	99	8.4	1905	4	US-09-252-991A-14312	Sequence 14312, App
44	98	8.3	1593	4	US-09-540-236-563	Sequence 563, App
45	98	8.3	89047	4	US-09-596-002-34	Sequence 34, App

ALIGNMENTS

RESULT 1
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Sequence 139, App
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31. US3. CIP
CURRENT APPLICATION NUMBER: US/09/663, 600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191, 997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066, 677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069, 957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074, 121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081, 563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096, 116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099, 273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent .pm
SEQ ID NO 139
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig.peptide
LOCATION: 36..107
OTHER INFORMATION: Von Heijne matrix

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OTHER INFORMATION: score 5.69999980926514
; OTHER INFORMATION: seq ILGLILGLTIVA/ML
; NAME/KEY: polyA_signal
; LOCATION: 1302..1307
; NAME/KEY: polyA_site
; LOCATION: 1389..1400
US-09-663-600A-139

Alignment Scores:
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Score: 1174.00 Matches: 230
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Query Match: 100.00% Indels: 0
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Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPlySerSerTyrValGlyAlaSerIle 40
Db 96 ACACGTGTCCTGACATGCTGCTCCACAGTGAACAAATCTTATGTCGGTGCACGACAT 155
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Qy 101 GlyMetArgGlyThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db 336 GGCATGAGATGACAGATCTTCTCCAGAGAAATCCGACACAAAGACAGATGGCGGTAGCA 395
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RESULT 2
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; Sequence 491. Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
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APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Inc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 491
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-002-491

Alignment Scores:
Pred. No.: 3.64e-142 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-787-677A-3 (1-230) x US-10-140-002-491 (1-1475)
Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGGCCCTCAACTTGTGGCTACATCTTAGCCCTTGGGGCTTTGGGC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrPlySerSerTyrValGlyAlaSerIle 40
Db 182 ACACGTGTCCTGACATGCTGCTCCACAGTGAACAAATCTTATGTCGGTGCACGACAT 241
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGATGTGGCTTCTCCAGAGGCTCTGATGAGATGTGCCACACACAGCAGGC 301
Qy 61 IleThrGlnCysAplIleTyrSerThrLeuGlyLeuProAlaAplIleGlnAla 80
Db 302 ATCAACCCAGTGTACATCTATAGACCCCTTCTGGGCTGCCCGGTGACATCCAGGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 362 CAGGCCATGATGTGACATCCAGATCTCTCCCTGGGCTCATTAATCTGTGTGTC 421
Qy 101 GlyMetArgGlyThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATGAGATGACAGATCTTCTCCAGAGAAATCCGACACAAAGACAGATGGCGGTAGCA 481
Qy 121 GlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTyrAsnLeu 140
Db 482 GGTGGATCTTTTTCATCTTGGAGGCTCTCTGGATTCATCTCTGTGCTGGAATCTT 541
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 542 CATGGATCTTACCGGACCTTCTACTCACACTGTGTGCTGCACAGCATGAATTTGAGATT 601
Qy 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGAGCTCTTAACTTGGGATTAATTTCTTCTCTCCCTGATGATGGAATATATC 661
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QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCCTGCTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACACATGCTTCCAGGCC 721
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValLysSerGlu 220
DB 722 CAACCTCTTGCCCAAGAGAGCTCTCCAGAGCTGTGTAACCTCCCAAGTCAAGAGTGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCATTCTACAGAGCTGACAGAGGTATGTC 811
RESULT 3
US-09-663-600A-45
Sequence 45, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleit, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 45
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 160..231
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6399980926514
NAME/KEY: polyA_signal
LOCATION: 1510..1515
NAME/KEY: polyA_site
LOCATION: 1506..1519
NAME/KEY: misc_feature
LOCATION: 1048..1504
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA552647
NAME/KEY: misc_feature
LOCATION: 597..846
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA345449
NAME/KEY: misc_feature
LOCATION: 39..53
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA345449
NAME/KEY: misc_feature
LOCATION: 113..149
OTHER INFORMATION: homology

OTHER INFORMATION: id: AA345449
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 98..400
OTHER INFORMATION: homology
OTHER INFORMATION: id: T86266
NAME/KEY: misc_feature
LOCATION: 1210..1489
OTHER INFORMATION: homology
OTHER INFORMATION: id: T86158
NAME/KEY: misc_feature
LOCATION: 954..983
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA116709
OTHER INFORMATION: est
US-09-663-600A-45
Alignment Scores:
Pred. No.: 1,39e-140 Length: 1524
Score: 1162.00 Matches: 228
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 2
Query Match: 98.98% Indels: 0
DB: 4 Gaps: 0
US-09-787-677A-3 (1-230) x US-09-663-600A-45 (1-1524)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
DB 160 ATGGCTCTTGGCTTCCCACTTGTGGCTACATCTAGGCTTCTGGGGCTTTGGGC 219
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
DB 220 ACAGTGTTGCCATGTGCTGCCCACTGGAAACAAGTTCTTATGCGGTGCAGCAT 279
QY 41 ValThrAlaValGlyPheSerTyrGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
DB 280 GTGACAGAGTGTGGCTTCTCCAGAGGCTCTGTGATGGAATGTCCACACACAGCAGGC 339
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 340 ATCACCAGGTGACATCTATAGCACCTTGTGGCTGCGCTGACATCCAKGCTGCC 399
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 400 CAGGCCATATGTGTGATCATCTCACTGCAATCTCTCCCTGGCTGCAATTATCTGTGGTG 459
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
DB 460 GGCATGATGATGACACATCTTCTCCAGGAATCCCGAGCCAAACAGAGTGGCGGTAGCA 519
QY 121 GlyGlyValPheHeIleLeuGlyIleLeuGlyPheIleProValAlaTyrAsnLeu 140
DB 520 GGTGAGTCTTTTCATCTTGGAGGCTCTGGAATCAATCTCTGTGCTGGAATCT 579
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 580 CATGGATCTTACGGAGACTTCTACTCACTGCTGCTCAGCATGAATTTGAGATT 639
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 640 GGAGAGGCTCTTACCTGGGCAATTATCTTCCCTGTCTCCCTGATGAGTGAATCATC 699
QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 700 CTCCTGCTTTCCGCTCATCTCCAGAGAAATCGCTCCAACTACACATGCTTCCAGGCC 759
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValLysSerGlu 220
DB 760 CAACCTCTTGCCCAAGAGAGCTCTCCAGAGCTGTGTAACCTCCCAAGTCAAGAGTGAG 819

QY	221	Pheanserlyrserleuthrglytyrval	230
DB	820	TTCAATTCTACAGCTGACAGGATATGTC	849

QY	141	Htsglylileuaurghaphehyrserproleuval	160
DB	603	CACAACATATCATCAAGCTTTCTACATCCGCTGAGCCCTCCGAGCAAGCGGAGATG	666

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QY      161 GlyGuaAlaLeuTyLeuGlyLeIleIleSerSerLeuPheSerLeuIleAGIyIleIle 160
Db      663 GGTGCTCGCTTACTAGTCGGCTGGGCGCGCTCCGCGCTGCTCTCTTCTTGCGGGGGGGCTG 722
QY      161 LeuCyPheSerCySeSerSerGlnArgAnaArgSerAenTyTyTAspAlaTyGlnAla 200
Db      723 CTTTCTGCAACTGTCCACCCCGCACACAGCAAG-----CCTTACTCCGCC 767
QY      201 GlnProLeuAlaThrArgSerSer 208
Db      768 AAGATTCGTGCTGCCCTCTGCT 791

RESULT 5
US-09-205-258-106
/ Sequence 106, Application US/09205258
/ Patent No. 6525174
/ GENERAL INFORMATION:
/ APPLICANT: Young et al.
/ TITLE OF INVENTION: 207 Human Secreted Proteins
/ FILE REFERENCE: P2007P1
/ CURRENT FILING DATE: US/09/205,258
/ EARLIER APPLICATION NUMBER: PCT/US98/11422
/ EARLIER FILING DATE: 1998-06-04
/ EARLIER APPLICATION NUMBER: 60/048,885
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,375
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,881
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,880
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,896
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,020
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,876
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,895
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,884
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,894
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,971
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,964
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,882
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,899
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,893
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,900
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,901
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,019
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,992
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,915
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,019
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,970
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,972
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,916
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,373
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,875

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QY 1 MetAlaserleuGlyleuGlnleuValGlyTyrIleleuGlyleuGlyleuGly 20
DB ATGGCCCTCTCCGGAGATGCAATCTCTGAGTCTCTGACACTGCTGGGTGGTAAAT 105
QY 21 ThrleuValAlaMetleuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
DB 106 GGCCCTGCTCTCTGCTGGCCCTGATGAGAGGATGACCGCTTTCATCGGACACGATC 165
QY 41 ValThrAlaValGlyPheSerIleGlyleuTrpMetGluCysAlaThrIleSerThrGly 60
DB 166 GTGGTGGCCAGAGGTGTGGAGAGGCGCTGTGATGTCTGCTGTGGTGCAGAGACGGC 225
QY 61 IleThrGlnCysAapIleTyrSerThrleuGlyleuProAlaAapIleGlnAla 80
DB 226 CAGATGACGTGCAAGGTGATGACACTGCTGCGCCCTGCACAGACCTGCAGGCTGCA 285
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
DB 286 CGTGCCCTCTGTGCTATCGCCCTCTGTGGCTCTGTGGCTGTGCTGCTGCTGCT 345
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAlaValAla 120
DB 346 GGGGCCCAAGGTATCACCTGTGTGAGAGAGAGATTCCAGAGCCGCTGTGCTCAAC 405
QY 121 GlyGlyValPhePheIleleuGlyleuGlyleuGlyPheIleProValAlaTrpAsn 140
DB 406 TCTGGATTGTCTTGTGATCTCAGGGGTCTGACCTGATCCCTGTGCTGCTGACGGC 465
QY 141 HisGlyIleleuArgAapPheTyrSerProleuValProApsSerMetLysPheGlu 160
DB 466 CAGTCCCTATCCGAGACTTCTATACCCCTGTGTGCTGAGCCCAAGCGGAGCTG 525
QY 161 GlyGlnAlaLeuTyrleuGlyIleIleSerSerleuPheSerleuIleAlaGlyIle 180
DB 526 GGGGCCCTCCCTATCTGTGGGTGGCGGCTGAGCCCTTTGTGTGCTGGGTGGGTG 585
QY 181 LeuCyApsPheSerCysSerSer-----GlnArgAsnArgSerAsnTyrTyrAspAlaTyr 198
DB 586 CTGTGCTGCACTTCCCTCGGGGGGTCCAGAGGCCCCCAAGCCATTACATGCGCCGCTAC 645
QY 199 GlnAlaGlnProleuAlaThrArgSerSerPro 209
DB 646 TCAACATCTGCGCCCTGCACTCTCGGGGGGCC 678

RESULT 7
US-09-673-395A-71
Sequence 71, Application US/09673395A
GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS
APPLICANT: HINZMANN, BERND
APPLICANT: SCHMITT, ARMIN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
FILE REFERENCE: ABRF-12
CURRENT APPLICATION NUMBER: US/09/673,395A
NUMBER OF SEQ ID NOS: 637
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 71
LENGTH: 1253
TYPE: DNA
ORGANISM: Homo sapiens
US-09-673-395A-71

Alignment Scores:
Pred. No.: 1,15e-45 Length: 1253
Score: 430.00 Matches: 88
Percent Similarity: 58.80% Conservative: 49
Best Local Similarity: 37.77% Mismatches: 83

Query Match: 36,63% Indels: 13
DB: 4 Gaps: 4
US-09-787-677A-3 (1-230) x US-09-673-395A-71 (1-1253)

QY 1 MetAlaserleuGlyleuGlnleuValGlyTyrIleleuGlyleuGlyleuGly 20
DB ATGGCCCTCTCCGGAGATGCAATCTCTGAGTCTCTGACACTGCTGGGTGGTAAAT 105
QY 21 ThrleuValAlaMetleuLeuProSerTrpIleThrSerSerTyrValGlyAlaSerIle 40
DB 106 GGCCCTGCTCTCTGCTGGCCCTGATGAGAGGATGACCGCTTTCATCGGACACGATC 165
QY 41 ValThrAlaValGlyPheSerIleGlyleuTrpMetGluCysAlaThrIleSerThrGly 60
DB 166 GTGGTGGCCAGAGGTGTGGAGAGGCGCTGTGATGTCTGCTGTGGTGCAGAGACGGC 225
QY 61 IleThrGlnCysAapIleTyrSerThrleuGlyleuProAlaAapIleGlnAla 80
DB 226 CAGATGACGTGCAAGGTGATGACACTGCTGCGCCCTGCACAGACCTGCAGGCTGCA 285
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
DB 286 CGTGCCCTCTGTGCTATCGCCCTCTGTGGCTCTGTGGCTGTGCTGCTGCTGCT 345
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAlaValAla 119
DB 346 GGGGCCCAAGGTATCACCTGTGTGAGAGAGAGATTCCAGAGCCGCTGTGCTCAAC 405
QY 121 GlyGlyValPhePheIleleuGlyleuGlyleuGlyPheIleProValAlaTrpAsn 139
DB 406 TCTGGATTGTCTTGTGATCTCAGGGGTCTGACCTGATCCCTGTGCTGCTGACGGC 465
QY 140 LeuHisGlyIleleuArgAapPheTyrSerProleuValProApsSerMetLysPheGlu 159
DB 706 GGGGCCCTCCCTATCTGTGGGTGGCGGCTGAGCCCTTTGTGTGCTGGGTGGGTG 765
QY 160 IleGlyGlnAlaLeuTyrleuGlyIleIleSerSerleuPheSerleuIleAlaGlyIle 179
DB 766 GGGCCATGATGTGACAGACTTATACCTTGTATCTCTTACCAATTAAGATGAG 825
QY 826 TTGGCCCTGCATCTTATTTGGGTGGCAGGGTCTGCTGATCATCTCGGAGGTGCA 885
QY 180 IleleuCyApsPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGln 199
DB 886 CTGCTCTCTGCTGTCTGTGGATGAGAGAGAGAGCTGATAC----- 930
QY 200 AlaGlnProleuAlaThrArgSerSerProArg-ProGlyGlnProProValLysSe 219
DB 931 -----CGTGACCCCGCTCTTACCTTAAGTCA---ACTCTTCAAGAGATATGTG 978
QY 219 rGluPheAsnSer-----TyrSerleuThrGlyTyr 229
DB 979 TGACCTGGATCTCTTCCCGCCAGCTGACAGGCTAT 1015

RESULT 8
US-09-895-652A-14
Sequence 14, Application US/09895652A
Patent No. 6774223
GENERAL INFORMATION:
APPLICANT: Macina, Roberta
APPLICANT: Pillai, Rageswari
TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and
FILE REFERENCE: DEX-0211
CURRENT APPLICATION NUMBER: US/09/895,652A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 60/214,515
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 1554
TYPE: DNA
ORGANISM: Homo sapiens


```

; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1544)
US-09-895-652A-14

Alignment Scores:
Pred. No.: 1,78e-44 Length: 1554
Score: 422.00 Matches: 89
Percent Similarity: 57.94% Conservative: 46
Best Local Similarity: 38.20% Mismatches: 86
Query Match: 35.95% Indels: 12
DB: 4 Gaps: 3

US-09-787-677A-3 (1-230) x US-09-895-652A-14 (1-1554)
QY 1 MetAlaserleuglyleuglnleuValGlyTYrilleuglyLeuLeuglyleuLeugly 20
Db 434 ATGGCCAAATTCGGGCTCGAGTTGCTGGCTTCATCGAGGCGCTGCGGCTGGGCTGGG 493
QY 20 YrHrleuValAlaMetleuLeuProSerTTPlyrThrSerSerTyValAlaSerIl 40
Db 494 TCTGGTGGCTGACCGCATCCCGCAGTGCAGATGAGCTCCTATGCGGGTGACACAT 553
QY 40 eValTrAlaValAlGlyPheSerlysglyLeuTPMeGluCyAlaLthrHisSerThrl 60
Db 554 CATCAGCGCCAGCCCATGTACAGGGGCTGTGGATGACTGCTCAGCAGACAGCGG 613
QY 60 YlIeThrGlnCyAspIleTySerThrleuLeuglyLeuProAlaAspIleGlnAla 80
Db 614 GATGATGAGCTGCAAAATGTACACTCGCTGCTGCCCTCGCCGCGCTTCAGCGCAC 673
QY 80 aglnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
Db 674 TCCAGCCCTATGCTGTCTCTCCCTGCGCTGCGCTTCCTCTCTGTCATTTGTGGCAGAT 733
QY 100 lGlyMetArgCyethrValPheCysGlnIuserArgAlaAsp---ArgValAla 119
Db 734 GGGCATGAAAGTGAAGCGGCTGTGGGGGAGACAGCAAAAGTGAAGAGCCCGTATAGCCAT 793
QY 119 lAlaGlyValAlaPhePheIleleuglyLeuLeuglyPheIleProValAlaTPAs 139
Db 794 GGGTGAAGGATATTTTATCGTGGCAGGCTTTGCCGCTGTGTACTGCTCTCGTA 853
QY 139 nLeuHlsglylLeuArgAspPheTySerProleuValProAspSerMetCysPheG 159
Db 854 TGGCCATCAGATTGTGACAGACTTTTATACCTTTGATCCCTTACCAACTTAAGTATGA 913
QY 159 uIlleGlyValAlaLeuTyrlleuglylIleIleSerSerleuPheSerleuIleAlaGly 179
Db 914 GTTGGCCCTGCAATCTTATATGCTGGGCAAGGCTGCTCCCTACTACTCCTGGAGGTGC 973
QY 179 eIlleuCyAspPheSerCysSerSerGlnArgAsnArgSerAsnTy---TyAspAla 198
Db 974 ACTGCTCTCTGTTCTCGTCTCGGAGTGAAGAGCAAGCGTGGTACCGTACCCGCTC 1033
QY 198 YrGlnAlaGlnProleuAlaLthrArgSerSerProArgProGlyGlnProProlyVal 218
Db 1034 TTACCCATAGTCCAAACTCTTCAAGGAGTATGTGTGACTGGGATCTCC----- 1083
QY 218 YrSerGlnPheAsnSerTySerSerleuThrGlyTy 229
Db 1084 -----TGCCCAAGCTGACAGACTAT 1104

RESULT 9
US-09-886-683A-3
; Sequence 3. Application US/0988683A
; Patent No. 6627439
; GENERAL INFORMATION:
; APPLICANT: Hoevel, Thoresten
; APPLICANT: Koch, Stefan
; APPLICANT: Kubbies, Manfred
; APPLICANT: Mundigl, Olaf
; APPLICANT: Rueger, Petra

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; TITLE OF INVENTION: Antibodies against SEMP1 (p23)
; FILE REFERENCE: Case 20692
; CURRENT APPLICATION NUMBER: US/09/886,683A
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: EP00113344.6
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: EP01107799.7
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (221) ..(853)
US-09-886-683A-3

Alignment Scores:
Pred. No.: 5.01e-42 Length: 3443
Score: 407.50 Matches: 81
Percent Similarity: 56.22% Conservative: 41
Best Local Similarity: 37.33% Mismatches: 78
Query Match: 34.71% Indels: 17
DB: 4 Gaps: 2

US-09-787-677A-3 (1-230) x US-09-886-683A-3 (1-3443)
QY 1 MetAlaserleuglyleuglnleuValGlyTYrilleuglyleuLeuglyleuLeugly 20
Db 221 ATGGCCAAAGCGGGGCTGACGCTGTGGCTTATTCGCTTCCTCGGATGAGATCGG 280
QY 21 ThleuValAlaMetleuLeuProSerTTPlyrThrSerSerTyValAlaSerIlle 40
Db 281 GCGATGTGACGACCTGCCCTGCCAGTGGAGATTATCTTCATGCGGCGGCAACATC 340
QY 41 ValThAlaValAlGlyPheSerlysglyLeuTPMeGluCyAlaLthrHisSerThrl 60
Db 341 GTACCGGCCAGCCCATGTACAGGGGCTGTGGATGCTCCGCTGTGCGCAGACACCGG 400
QY 61 lIeThrGlnCyAspIleTySerThrleuLeuglyLeuProAlaAspIleGlnAla 80
Db 61 lIeThrGlnCyAspIleTySerThrleuLeuglyLeuProAlaAspIleGlnAla 80
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerleuAlaCysIleIleSerVal 100
Db 401 CAGATCCAGTGAAGCTTTGACTCTTGCTGAATCTGAGCAGCATTGCAAGCAACC 460
QY 461 CGTGCCTTGAATGCTGTGGCATCTTCCTGGAGTGAATGACATCTTGTGGCAGCGTT 520
QY 101 GlyMetArgCyethrValPheCysGlnIuserArgAla---LysAspArgValAlaVal 119
Db 521 GGCATGAAGTGTGAAGTCTTGGAAAGCATGAGAGTGCAGAGATGAAGATGGCTGTC 580
QY 120 AlAGlyValAlaPhePheIleleuglylLeuLeuglyPheIleProValAlaTPAsn 139
Db 581 ATGGGGGGTGCATATTTCTTTCGACAGTCTGCTATTTATTTATGTGACAGATGGTAT 640
QY 140 LeuHlsglylLeuArgAspPheTySerProleuValProAspSerMetCysPheG 159
Db 641 GGGCAATGAATCTTCAAGATTTCTATGACCTATGACCCATGCAATGCGAGTAGAA 700
QY 160 lIleGlyValAlaLeuTyrlleuglylIleIleSerSerleuPheSerleuIleAlaGly 179
Db 701 TTTGGTCAAGGCTCTTCACTGCTGGCTGGCTGTCTCTCTGCTTCTGAGAGGTGCC 760
QY 180 lIleuCyAspPheSerCysSerSerGlnArgAsnArgSerAsnTyTyAspAlaTyGln 199
Db 761 CTACTTGTCTGTTCTCT----- 778
QY 200 AlAGlnProleuAlaLthrArgSerSerProArgProGlyGlnProProlyVal 216
Db 779 -----CCCCGAAAACCAACTCTTACCCACACCAAGGCCCTATCCAAA 823

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RESULT 10
US-09-130-491-3
Sequence 3, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT FILING DATE: US/09130, 491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058, 108
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054, 961
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 3483
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (240) ... (872)
US-09-130-491-3

Alignment Scores:
Pred. No.: 5.1e-42 Length: 3483
Score: 407.50 Matches: 81
Percent Similarity: 56.22% Conservative: 41
Best Local Similarity: 37.33% Mismatches: 78
Query Match: 34.71% Indels: 17
DB: Gaps: 2

US-09-787-677A-3 (1-230) x US-09-130-491-3 (1-3483)
QY 1 MetAlaSerLeuGlyLeuGlnInLeuValAlaGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 240 ATGGCCAAAGCGCGGGGTGACGCTGTTGGGCTTATCTCCCTTCCTGGGATGGATGGC 239
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValAlaSerIle 40
Db 300 GCCATCGTCAGACACGCCCTGGCCCAAGTAGAGATTATCTCCATGCGCGGCAACATC 359
QY 41 ValIrrAlaValAlaGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 360 GTGACCGCCCAAGCCCATGTACGAGGGGCTGTGATGCTCGCGTGCAGACACCGGG 419
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaIle 80
Db 420 CAGATCCAGTGCAGAAAGCTTTGACTCTGCTGCTGAATCTGAGACGACATGGCAAGCAC 479
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValIle 100
Db 480 CGTGCTGTGATGTGTGGTTGGCATCCCTCCGAGAGTAGATACCATCTTTGGGCCACCGTT 539
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAla--LysAspArgValAlaVal 119
Db 540 GGCATGAAGTGTATGAAAGTGTGGGAAGACGATGAGGTGCAGAAAGATGAGGATGGCTGC 599
QY 120 AlaGlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaIleProAsn 139
Db 600 ATGGGGGGCGCATATTTCTTCTTGGACGGCTGTGCTATTTTATGTGACACGACATGGTAT 659
QY 140 LeuHisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlu 159
Db 660 GGCATAGATGATGTTTAAAGATTTCTATGACCTATGACCCCAAGTCAATGCCAGTAGAA 719
QY 160 IleGlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 179
Db 720 TTGTGCAAGCTCTCTTCACTGGCTGGGCGTGGCTTCTGCTTGGCGCTTGGGAGTGCC 779
QY 180 IleLeuCysPheSerCysSerSerGlnAlaArgAsnArgSerAsnTyrTyrAspAlaTyrGln 199

```

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Db      780 CTACTTCTGTTCTGT-----              797
Qy      200 ALAGINProLeuAlaThrArgSerProArgProGIynProProlys   216
          |||||
          |::|
          -----CCCCGAACCAACCATTACCCACAAGAAGCCTATTCANAA    842
Db

RESULT 11
US-09-489-847-93
/ Sequence 93, Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: PZ031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ CURRENT FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ EARLIER FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: Patentin Ver. 2.0
/ SEO ID NO 93
/ LENGTH: 1722
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-489-847-93

Alignment Scores:
Pred. No.:           6e-39             Length:        1722
Score:               380.00            Matches:         79
Percent Similarity:  57.45%            Conservative:     56
Best Local Similarity: 33.62%          Mismatches:       82
Query Match:         32.37%            Indels:           18
DBs:                  4                 Gaps:            4

US-09-787-677A-3 (1-230) x US-09-489-847-93 (1-1722)
Qy      1 MetaLasertleuglyLeuglinleuvaIgiTyrlileLeuglyLeuleuglyLeuleugly
Db      461 ATGGGCGTGCGAGCGCTTGGAGATcctggcccggtgnccttgcttggatgggcctggagggt
Qy      21 ThirleuvaiJalmetleuleuproserTrplyrThrsersetryValglalaserrlle
          ::::::|
Db      521 CTAATCCGTGCCTGCGGGGCTGCCCATATGTGGCAGGTGACCGCCTTCTGTGACCCAACATC
          |||||||
Qy      41 ValTHRAALaVALGLYphesertrysgilyLeutTPMeGlucYAalaahrtisserngly
          :|||
Db      581 GTGACGGCGCACAGCAACCTGTGAAGGGCGGTGTGATGTCGTGCTGTGACAGACAGSGGS
          |||||
Qy      61 IletnrgInCYeaSPILetysierThrtleueuglyLeuPROAlasplieGINALAIA
          |||||
Db      641 CAcatGCAGTGCMAAgTGTAcacacttcggtcgtgccctTAGACAGCAGGTGACGSGCGC
          |||||
Qy      101 GIyletarCyGrThVAlpheCyseIngIUSeRgaLaLyehapgrYaVaIALaVAIA
          ::::::|
Db      761 GGCGGCGCaGTGaCCaCcTGTGCGCCCGGGCCCGGCGCAAGCGGTGTGGCCCTCACG
          ::::::|
Qy      121 GIylgyValIphePhelILEuendlyGIlyLeuleuglyPhelIProvaIMAtTpAnleU
          |||||
```

Db 821 GGAGGCGTCTACCTGTTTTCGGGGCTGCTGGCGCTGCTGCGACCTCTGTTGCC 880
Qy 141 HhAGLYlleuAargAspPheTYrSerProLeuValProAspSerMetLysPheGluIle 160
Db 881 AACATTGCTGCTCGCGAGTTTACGACCCGCTGCTGCTGCTGCGAGAGTACGAGCTG 940
Qy 161 GYGLuAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAglIleIle 180
Db 941 GGGCGAGCGTGTACATCGCTGCGGGCCAGCCGCTGCTCATGTAGGCGGCTGCTC 1000
Qy 181 LeuCyS-----PheSerCySerSerGlnAargSerAsnTYrTYrAspAla 197
Db 1001 TTGTGCTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1057
Qy 198 TYrGlnAla-----GlnProLeuAlaThrArg----- 206
Db 1058 TACTCAGCG 1117
Qy 207 -----SerSerProArgProGlyGlnProProLysValLys 218
Db 1118 GGGCGCTGGGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1162
RESULT 12
US-09-489-847-125
Sequence 125, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031P1
CURRENT APPLICATION NUMBER: US/09/489, 847
EARLIER FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094, 657
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095, 486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096, 319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095, 454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095, 455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 125
LENGTH: 1380
TYPE: DNA
ORGANISM: Homo sapiens
US-09-489-847-125
Alignment Scores:
Pred. No.: 3 93e-33 Length: 1380
Score: 334.00 Matches: 78
Percent Similarity: 57.02% Conserved: 56
Best Local Similarity: 33.19% Mismatches: 83
Query Match: 28.45% Indels: 20
DB: 4 Gaps: 4
US-09-787-677a-3 (1-230) x US-09-489-847-125 (1-1380)
Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTYrIleLeuGlyLeuGlyLeuGlyLeuGly 20
Db 135 ATGGGGTCCCGACGCTTGAGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 194
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTYrValAlaSerIle 40
Db 195 CTGATCTGTGGCG 254
Qy 41 ValThrAlaValAlaGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 255 GTATCGCGCGACGACCACTGGAAGGGGCTGTGATGTGCTGCTGCTGCTGCTGCTG 314

Qy 61 IleThrGlnCysAspIleTYrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaIle 80
Db 315 AC-ATGCACTGTGCAAAATGTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 374 CGGGCGCTACCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 433
Qy 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaVal 120
Db 434 GGGCGCAGTGCACCACTGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 493
Qy 121 GYGLYValAlaPheMetIleLeuGlyIleLeuGlyLeuGlyPheIleProValAlaTrpLeu 140
Db 494 GGAGGCTGCTCTACCTGTTTTCGGGCTGCTGCGCTGCTGCTGCTGCTGCTGCTG 553
Qy 141 HhAGLYlleuAargAspPheTYrSerProLeuValProAspSerMetLysPheGluIle 160
Db 554 AACATTGCTGCTCGCGAGTTTACGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
Qy 161 GYGLuAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAglIleIle 180
Db 614 GGGCG-ACGCTGTACATCGCTGCGGGCCAGCCGCTGCTCATGTAGGCGGCTGCTC 672
Qy 181 LeuCyS-----PheSerCySerSerGlnAargSerAsnTYrTYrAspAla 197
Db 673 TTGTGCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729
Qy 198 TYrGlnAla-----GlnProLeuAlaThrArg----- 206
Db 730 TACTCAGCG 789
Qy 207 -----SerSerProArgProGlyGlnProProLysValLys 218
Db 790 GGGCGCTGGGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 834
RESULT 13
US-09-603-552-2
Sequence 2, Application US/09603552
Patent No. 6590089
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE
FILE REFERENCE: PG-0016 US
CURRENT APPLICATION NUMBER: US/09/603, 552
EARLIER FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 1165
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6590089 1456746CB1
US-09-603-552-2
Alignment Scores:
Pred. No.: 1.01e-30 Length: 1165
Score: 314.50 Matches: 78
Percent Similarity: 52.08% Conserved: 47
Best Local Similarity: 32.50% Mismatches: 90
Query Match: 26.79% Indels: 25
DB: 4 Gaps: 10
US-09-787-677a-3 (1-230) x US-09-603-552-2 (1-1165)
Qy 3 SerLeuGlyLeuGlnLeuValGlyTYrIleLeuGlyLeuGlyLeuGlyLeuGlyLeu 22
Db 325 TCATAGCTGTGTGAACCTTTTGCTTTCATGAGCAACTGTGTGGGCTGCTG-----ATG 378

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QY 23 ValAlaMetLeuProSer-----TrpIleThrSerSerTyValAlaSerIle 40
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 379 CTGGGGGTGACTGCGAAACAGTACTGAGTGTCTCACT---GGTACGGGAGTGC 435
QY 41 ValThrAlaValGlyPheSerTyGlyLeuTrpMetGluCysAlaThrHisSerThyl 60
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 436 ATCAACCCACCAACCACTTCCAGAACCTCTGTGTTAGCTGTGCACCACTCCCTGGC 495
QY 61 IleThrGlnCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 496 GTCTACAACTGCTGGAGTTCCTCCCATGCTGGCCCTCTGTGGGTATATTCAGGCTGC 555
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 556 CGGCACTCATGATACACCGCCATCTCTGGGCTTCTCGGCTCTTGAGCATCGG 615
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaVal 120
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 616 GGCCTGGCTGCACCAACATT-----GGGGCTGTGAGCTCTCCAGGAAAGCTCAAGCT 669
QY 121 GlyGly-----ValPhePheIleLeuGlyIleLeuGlyIleLeuGlyIleProVal 137
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 670 GGGGGCCACCGCAGGGCCCTCCACATTCGTGGCGGTATCTGGGGATGTGGCCATCTCC 729
QY 138 TrpAsnLeuHisGlyIleLeuArgAspPheTySerProLeuValProAspSerMet 157
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 730 TGTGACCGCTTCAACATACACCGGACTTCTTCACACCTGTGATCCCGGAAAC--AAG 786
QY 158 PheGluIleGlyGlnAlaLeuTyLeuGlyIleIleSerSerLeuPheSerIleAla 177
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 787 TAGCAAGTGGGCCCCGCCCTTACTGTGGGTGAGGCCCTCACATCTCATCTGGGT 846
QY 178 GlyIleIleLeuCysPheSerCys-----SerSerGlnArgAsnArgSerAsnTy 194
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 847 GGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
QY 195 TyrAspAlaTyrglnAla-----GlnProLeuAlaThrArgSerProArg 210
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 907 CGCGCGCCCTTACAGGCTCCAGTCCGTGATGCCGCTGCCACCC-----TCGGACCA 960
QY 211 ProGlyGlnProProlyValIleSerGluPheAsnSerTySerLeuThrGlyTyVal 230
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 961 GAAGGCGAC-----AGCAGCTTGGCAATACGGCAGAAAGCCCTAGGTG 1005

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DB: 3 Gaps: 4
US-09-787-677a-3 (1-230) x US-09-724-864-32 (1-1353)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyTrpIleLeuGlyLeuLeuGlyLeu 20
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 136 ATGGCCACCAACAGTCCAGGTGTGTAGGGCTTCTCTGCTCCCTCCGCTGGGTGCGCGC 195
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpIleThrSerSerTyValAlaSerIle 40
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 196 TGTACACCCCGCCACTGGAGTGAACATGTGAGAGCACTTACAGACCTGTATGAC--AACCA 252
QY 41 ValThrAlaValGlyPheSerTyGlyLeuTrpMetGluCysAlaThrHisSerThyl 60
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 253 GTCAACCCCTGTTCACGATGAGAGGCTTGTGAGAGATTCCTGTCACAGACACTCGGG 312
QY 61 IleThrGlnCysAspIleTySerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 313 TTCACGAGTGGCGGCATCTTACCATCTGCGGCTTCCAGCAATGCTGCAAGCTGTA 372
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 373 CGAGCCTGATGATCTGGGCACTTCTGGGGGTCTCATGCTGCTGCTCATCTTC 432
QY 101 GlyMetArgCys--ThrValPheCysGlnGluSerArgAlaIleAspArgValAlaVal 119
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 433 GGCCTGAGTCACTTGCATGTGTAGCATGATGATGATGATGATGATGATGATGATG 492
QY 120 AlaGlyIleValPhePheIleLeuGlyIleLeuGlyIlePheIleProValAla----- 137
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 493 ACTTGTGGATCTTGTTCATCATCTCCGCGCATCTGTGCAATCATTTGGTGTGTGTGTT 552
QY 138 -----Trp-----AsnLeuHisGlyIleLeuArg 145
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 553 GCCAACATGCTGTGACCACTTCTGTAGTGTCCACAGTAACTGATGACGGGCAATGGC 612
QY 146 AspPheTySerProLeuValProAspSerMetLeuPheGluIleGlyGlnAlaLeuTy 165
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 613 GGCATGTGTGCGCATGTCGACGACCTTCCAGACAGATGACACTTGGGTGAGCTCTTC 672
QY 166 LeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIleLeuCysPheSerCys 185
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 673 GTGGGCTGGGTTCTGTGAGGCTTACCCCTGATTTGGGGAGTGTGATGATGATGATG 732
QY 186 SerSerGlnArgAsnArgSerAsnTyTyAspAlaTyrglnAlaGlnProLeuAlaThr 205
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 733 CTGGCCTGACACCAAGTATGACAGCACTTCAAGCTGTGTTCATTCATGCTCTGSCCA 792
QY 206 ArgSerSerProArgProGly 212
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 793 AATGTCCTTACAGGCTTGA 813

```

RESULT 14
 US-09-724-864-32
 : Sequence 32, Application US/09724864
 : Patent No. 6380362
 : GENERAL INFORMATION:
 : APPLICANT: Watson, James D
 : APPLICANT: Murison, James G.
 : TITLE OF INVENTION: Polynucleotides, polypeptides expressed
 : TITLE OF INVENTION: by the polynucleotides and methods for their use.
 : FILE REFERENCE: 11000.105001
 : CURRENT APPLICATION NUMBER: US/09/724,864
 : CURRENT FILING DATE: 2000-11-28
 : PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
 : NUMBER OF SEQ ID NOS: 72
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 32
 : LENGTH: 1353
 : TYPE: DNA
 : ORGANISM: Mouse
 : US-09-724-864-32

Alignment Scores:
 Pred. No.: 1.74e-25 Length: 1353
 Score: 275.00 Matches: 62
 Percent Similarity: 48.46% Conservative: 48
 Best Local Similarity: 27.31% Mismatches: 101
 Query Match: 23.42% Indels: 16

RESULT 15
 US-08-966-316-8
 : Sequence 8, Application US/08966316
 : Patent No. 5932445
 : GENERAL INFORMATION:
 : APPLICANT: Lal, Preeti
 : APPLICANT: Au-Young, Janice
 : APPLICANT: Reddy, Roopa
 : APPLICANT: Murty, Lynn E.
 : APPLICANT: Mathur, Preete
 : TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Incyte Pharmaceuticals, Inc.
 : STREET: 3174 Porter Drive
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94304
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS Windows Version 2.0
SOFTWARE: FastSeq for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HMTJAZT01
CLONE: 2417676
US-08-966-316-8

Alignment Scores:
Pred. No.: 7.75e-21 Length: 363
Score: 232.00 Matches: 44
Percent Similarity: 63.81% Conservative: 23
Best Local Similarity: 41.90% Mismatches: 38
Query Match: 19.76% Indels: 0
DB: 2 Gaps: 0

US-09-787-677A-3 (1-230) x US-08-966-316-8 (1-363)
QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGlyLeuGly 20
Db 48 ATGGCCCTCTCCCGAATGCAATCTCTGGAGCTCTCTGACACTGCTGGGCTGGTAAT 107
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrIleThrSerSerTyrValGlyAlaSerIle 40
Db 108 GGCCTGGTCTCTGTCGCCCTGCCATGTGAGAGTGACCGCTTCATCGGCACACGATC 167
QY 41 ValThrAlaValAlaGlyPheSerIleGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
Db 168 GTGTGTGCCCGAGGTGTGTGGAGGGCTGTGTGATGTCCTGCTGTGCAGAGCACCGGC 227
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db 228 CAGATGACAGTGCAGAGGTGATGACTGCTGTGGCGCTGCACAGACCTGCAGGCTGCA 287
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 288 CGTGCCCTCTGTGTGCATGCGCTCTGTGTGCGCTGTGTGCGCMTGTGTCTACTTGTCT 347
QY 101 GlyMetArgCysThr 105
Db 348 GGGGCCAAGTTTACC 362
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Search completed: December 20, 2004, 16:51:58
Job time: 98 secs

Gencore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 15:38:36 ; Search time 546 Seconds

(without alignments)

2325.628 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 1174

Sequence: 1 MASLGLVYIGLIGLIGL.....PGQPKVXSEFNSYSLTGYV 230

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 6186004

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09787677 @CGN_1_1 480 @runcat_20122004_132742_19497
-NCPU=6 -ICPU=3 -NO_MMAP -LARGESQUERY -NEG_SCORES=0 -MAIT -DSBLOC=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1174	100.0	1400	11	US-09-978-360A-56	Sequence 56, Appl
2	1174	100.0	1400	10	US-10-319-763-139	Sequence 139, App
3	1174	100.0	1475	10	US-09-888-257A-1	Sequence 1, Appl
4	1174	100.0	1475	10	US-09-946-374-133	Sequence 133, App
5	1174	100.0	1475	13	US-10-006-861-79	Sequence 79, Appl
6	1174	100.0	1475	13	US-10-063-547-79	Sequence 79, Appl
7	1174	100.0	1475	13	US-10-028-072-491	Sequence 79, Appl
8	1174	100.0	1475	14	US-10-063-616-79	Sequence 79, Appl
9	1174	100.0	1475	14	US-10-140-808-491	Sequence 491, App
10	1174	100.0	1475	14	US-10-063-589-79	Sequence 79, Appl
11	1174	100.0	1475	14	US-10-063-513-79	Sequence 79, Appl
12	1174	100.0	1475	14	US-10-063-515-79	Sequence 79, Appl
13	1174	100.0	1475	14	US-10-063-512-79	Sequence 79, Appl
14	1174	100.0	1475	14	US-10-121-049-491	Sequence 491, App
15	1174	100.0	1475	14	US-10-123-904-491	Sequence 491, App
16	1174	100.0	1475	14	US-10-140-470-491	Sequence 491, App
17	1174	100.0	1475	14	US-10-140-470-491	Sequence 491, App
18	1174	100.0	1475	14	US-10-063-512-79	Sequence 79, Appl
19	1174	100.0	1475	14	US-10-175-746-491	Sequence 491, App
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21	1174	100.0	1475	14	US-10-176-921-491	Sequence 491, App
22	1174	100.0	1475	14	US-10-063-548-79	Sequence 79, Appl
23	1174	100.0	1475	14	US-10-137-865-491	Sequence 491, App
24	1174	100.0	1475	14	US-10-140-474-491	Sequence 491, App
25	1174	100.0	1475	14	US-10-142-431-491	Sequence 491, App
26	1174	100.0	1475	14	US-10-143-114-491	Sequence 491, App
27	1174	100.0	1475	14	US-10-140-002-491	Sequence 491, App
28	1174	100.0	1475	14	US-10-063-554-79	Sequence 79, Appl
29	1174	100.0	1475	14	US-10-006-856A-133	Sequence 133, App
30	1174	100.0	1475	14	US-10-142-419-491	Sequence 79, Appl
31	1174	100.0	1475	14	US-10-063-553-79	Sequence 79, Appl
32	1174	100.0	1475	14	US-10-063-518-79	Sequence 79, Appl
33	1174	100.0	1475	14	US-10-123-262-491	Sequence 491, App
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41	1174	100.0	1475	14	US-10-063-563-79	Sequence 79, Appl
42	1174	100.0	1475	14	US-10-006-485A-133	Sequence 133, App
43	1174	100.0	1475	14	US-10-013-907A-133	Sequence 133, App
44	1174	100.0	1475	14	US-10-015-499A-133	Sequence 133, App
45	1174	100.0	1475	14	US-10-063-555-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-978-360A-56
Sequence 56, Application US/0978360A
Publication No. US20040110939A1
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Bougueleret, Lydie
APPLICANT: Joubert, Severin
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56. US4.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563

PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 56
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig.peptide
LOCATION: 36..107
OTHER INFORMATION: Von Heljne matrix
OTHER INFORMATION: score 5.6999980926514
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1302..1307
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1389..1400
US-09-978-360A-56

Alignment Scores:
Pred. No.: 2,26e-131 Length: 1400
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-787-677A-3 (1-230) x US-09-978-360A-56 (1-1400)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 36 ATGGCTCTCTGGCTTCCAACTTGAGGCTACATCCAGGCTTCTGGGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrIleSerSerTyrValGlyAlaSerIle 40
DB 96 ACACTGCTTGCATGCTGCTCCAGCTGGAACAAGTTCTTATGCGGTGCGCAGCAT 155
QY 41 ValThrAlaValGlyPheSerLeuGlyLeuTyrMetGluCysAlaThrHisSerThrGly 60
DB 156 GTGACAGCAGTGGCTTCTCCAGGCTCTGATGATGATGTCACACACAGCAGGC 215
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
DB 216 ATCCACCAAGTGTGATCTATAGCACCTTCTGGGCTGCGCGGTGACATCAGGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
DB 276 CAGGCTCATGATGGATCATCCAGTCAATCTCCCTGGGCTGCATTATCTGTGGTG 335
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAspArgValAlaValAla 120
DB 336 GGGCTGTGATGACACAGCTTCTGCGCAGGAATCCGAGCAAGACAGAGTGGCGGTAGCA 395
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
DB 396 GGTGGAGTCTTTTTCATCTCTGGAGGCTCTGGAATTCATCTCTGTGGTGAATCTT 455
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160

DB 456 CATGGATCTTACGGGACTTCTACTCACCACTGTGCTTACAGCATGAATTTGAGATT 515
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 516 GGAGAGGCTCTTACTTGGGCTATTTCTTCCCTGTTCCCTGATGCTGGATCATC 575
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 576 CTCTGCTTTTCCGCTCATATCCAGAGAAATCGCTCCAACTACATGCTTACCAAGCC 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
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DB 696 TTCATTTCTTACAGCTGACAGGCTATGTG 725

RESULT 2

US-10-319-763-139
Sequence 139, Application US/10319763
Publication No. US20030144490A1
GENERAL INFORMATION:
APPLICANT: Dumas MLine Edwards, Jean-Baptiste
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.US04.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 139
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig.peptide
LOCATION: 36..107
OTHER INFORMATION: Von Heljne matrix
OTHER INFORMATION: score 5.6999980926514
OTHER INFORMATION: seq ILGLLGLTLVA/ML
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1302..1307
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1389..1400
US-10-319-763-139

Alignment Scores:
Pred. No.: 2,26e-131 Length: 1400
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-787-677A-3 (1-230) x US-10-319-763-139 (1-1400)


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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
DB 36 ATGGCTCTCTTGGCTCCAACTTGAGGCTACATCTAGCCCTTGGGAGCTTTGGGC 95
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
DB 96 ACCTGGTTGCCATGGCTGCTCCCAAGCTGAGAAACAAGTTCTTATGTCGGTGGCAGATT 155
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 156 GTGACAGCAGATTGGCTTCTCCAAAGGCTCTGATGGAATGTCACACACAGCAGC 215
QY 61 IleThrGlnCysAspIleTySerThrLeuGlyLeuProAlaAspIleGlnAla 80
DB 216 ATACCCAGTGTACATCTATAGCACCTTCTGGGCTGCCCCCTGACATCCAGGCTGCC 275
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 276 CAGGCATGATGTGATCATCATCAGATCTCTCTCCCTGGCTGCAATATCTCTGTGCTG 335
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
DB 336 GGCATAGAGATGCACAGCTCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGCGTAGCA 395
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTrpAsnLeu 140
DB 396 GGTGGAGCTCTTTTCACTTGAAGGCTCTGGGATTCATTCCTGTGGCTGAATCTT 455
QY 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
DB 456 CATGGATCTTACGGAGCTTCTACTACACCTGTGCTGACAGCATGAATTTGAGATT 515
QY 161 GlyGlyAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
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DB 576 CTCTGCTTTTCCGCTCATCTCCAGAGAAATGCTCCCAACTACATGATGCTTCCAAAGCC 635
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
DB 636 CAACCTCTTGCCCAAGAGAGCTCTCCAGGCTGGTCAACCTCCCAAGCAAGAGAGGAG 695
QY 221 PheAsnSerTySerLeuThrGlyTyVal 230
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US-09-888-257A-1
/ Sequence 1, Application US/09888257A
/ Publication No. US20030060612A1
/ GENERAL INFORMATION:
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Polakis, Paul
/ APPLICANT: Smith, Victoria
/ APPLICANT: Wood, William I.
/ APPLICANT: Wu, Thomas D.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ FILE REFERENCE: P5002R1
/ CURRENT APPLICATION NUMBER: US/09/888,257A
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/063,540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: US 60/089,653
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: US 60/099,792
/ PRIOR FILING DATE: 1998-09-10

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/ PRIOR APPLICATION NUMBER: US 60/103,678
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: US 60/235,451
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: PCT/US99/12252
/ PRIOR FILING DATE: 1999-06-02
/ PRIOR APPLICATION NUMBER: PCT/US99/20111
/ PRIOR FILING DATE: 1999-09-01
/ PRIOR APPLICATION NUMBER: PCT/US00/04342
/ PRIOR FILING DATE: 2000-02-18
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: 2000-03-02
/ PRIOR APPLICATION NUMBER: PCT/US00/08439
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: PCT/US01/06666
/ PRIOR FILING DATE: 2001-03-01
/ NUMBER OF SEQ ID NOS: 10
/ SEQ ID NO 1
/ LENGTH: 1475
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-09-888-257A-1

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Pred. No.:	2,43e-131	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-787-677A-3 (1-230) x US-09-888-257A-1 (1-1475)
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QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
DB 182 ACCTGGTTGCCATGGCTGCTCCCAAGCTGAGAAACAAGTTCTTATGTCGGTGGCAGATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
DB 242 GTGACAGCAGATTGGCTTCTCCAAAGGCTCTGATGGAATGTCACACACAGCAGC 301
QY 61 IleThrGlnCysAspIleTySerThrLeuGlyLeuProAlaAspIleGlnAla 80
DB 302 ATACCCAGTGTACATCTATAGCACCTTCTGGGCTGCCCCCTGACATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCATGATGTGATCATCATCAGATCTCTCTCCCTGGCTGCAATATCTCTGTGCTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
DB 422 GGCATAGAGATGCACAGCTTCTGCGAGAAATCCCGAGCCAAAGACAGAGTGGCGTAGCA 481
QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuGlyPheIleProValAlaTrpAsnLeu 140
DB 482 GGTGGAGCTCTTTTCACTTGAAGGCTCTGGGATTCATTCCTGTGGCTGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGAGCTTCTACTACACCTGTGCTCCAGCAAGCATGAATTTGAGATT 601
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Db 602 GGAGAGCTTACTTGCGCATATTCTTCCTGTTCCCTGATAGTGAATCATC 661
Qy 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntYrTyraAlaIYrGlnAla 200
Db 662 CTCTGCTTTTCCGCTCATCCAGAGAAATCGCTCCAACTACATACATGCTTCCAGGCC 721
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 722 CAACCTCTTGCCACAGAGAGCTCTCCAGGCTTGCTCAACTCCCAAGTCAGAGTGAG 781
Qy 221 PheAsnSerTySerLeuThrGlyTyVal 230
Db 782 TTCAATTCCTACAGCTGACAGGATATGTG 811
RESULT 4
US-09-946-374-133
Sequence 133, Application US/09946374
Publication No. US2003073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
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PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1998-09-10

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PRIOR APPLICATION NUMBER: 60/101915

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PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102307
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103396
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103401
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103633
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PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores: 2.43e-131 Length: 1475
Pred. No.:

Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-787-677a-3 (1-230) x US-09-946-374-133 (1-1475)

QY 1 MetAlaSerLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
122 ATGGCTCTCTGGCTTCCCACTTGTGGCTTACCTAGGCTTCTGGGGCTTTGGGC 181
DB 21 ThrLeuValAlaMetLeuProSerTyrThrSerTyrValGlyAlaSerIle 40
182 ACACGTGTGCGACGTGCTCCAGCTGGAACAAAGTTTATATGCGGTGACGAT 241
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThy 60
242 GTGACAGCACTTGGCTTCTCCAGGGCTCTGATGGAATGTCCACACAGACAGGC 301
DB 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
302 ATCACCAGTGTGACATCTATACACCTTCTGGGCTGCGCTGCATCCAGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
362 CAGGCCATGATGATGATCATCATCATCTCTCCCTGCGCTGCATATCTCTGTGGT 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIleAspArgValAlaVal 120
422 GCGATGATGATGATGATCATCTTCTCCAGGATCCCGACCAACAGAGTGGCGTGCA 481
DB 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPasnLeu 140
482 GGTGAGTCTTTTCTTCTCTTCTGAGGCTCTCGGATTCATCTCTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGlu 160
542 CATGGATCTCTAGGAGCTTCTACTCACCTGCTGACAGCATGAATTTGAAATT 601
DB 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
602 GAGAGGCTCTTACTTGGCATTTATTTCTCTCTCTCTCTGATGATGATATATC 661
QY 181 LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
662 CTCTGCTTTTCTGCTCATCTCCAGAAATGCTCCAACTACTAGATGCTTCAAGCC 721
DB 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProlyValIleSerGlu 220
722 CAACCTCTTGCCCAAGAGAGCTCTCCAAAGGCTGTCAACTCCCAAGTCAAGAGT 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
782 TTCAATTCTTACAGCTGACAGGGTATGTG 811
DB

RESULT 5
US-10-006-867-79
; Sequence 79, Application US//10006867
; Publication No. US2002011910A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: WOOD, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1

CURRENT APPLICATION NUMBER: US/10/006,867
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/064215
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
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PRIOR APPLICATION NUMBER: 60/088030
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PRIOR APPLICATION NUMBER: 60/088734
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PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090696
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PRIOR APPLICATION NUMBER: 60/090862
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PRIOR APPLICATION NUMBER: 60/091628
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PRIOR FILING DATE: 1998-08-17
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PRIOR FILING DATE: 1998-08-26
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PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
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PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08
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PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105881
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/106030
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PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106856
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108807
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/112419
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112853
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PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/115614
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116527
PRIOR FILING DATE: 1999-01-20

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PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/119285
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119287
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PRIOR APPLICATION NUMBER: 60/129674
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PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/380139
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142

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Alignment Scores:

Pred. No.:	2,43e-131	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13	Indels:	0
DB:	13	Gaps:	0

US-09-787-677a-3 (1-230) x US-10-006-867-79 (1-1475)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
DB 122 ATGGCTCTCTTGGCTCCCACTTGCGCTACATCTTAGCGCTTCTGGGGCTTTGGG 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLySerTherSerTrpValGlyAlaSerIle 40
DB 182 ACCTGCTGTCCTGCTGCTCCCACTGGAAGAAACAGTTCTTAATGCGGTGCACGATT 241
QY 41 ValThrAlaValGlyPheSerTrpGlyLeuTrpMetGlyCysAlaThrHisSerThnGly 60
DB 242 GTACACGACATTGGCTTCTTCCAGGGCTCTGATGGAATGTGCCACACACAGCAGGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
DB 302 ATCACCACAGTGTACATCTATACACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCC 361
QY 81 GluAlaMetSerValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
DB 362 CAGGCCATGATGGTGAATCAGTGCATCTCTCCCTGCGCTGCATTAATCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGlySerArgAlaIleYsaSparValAlaValAla 120
DB 422 GGATAGATGACACAGTCTTCTGCGAGGAATCCGAGCCAAAGACAGAGTGGCGGTGCA 481

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QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPantLeu 140
DB 482 GGTGAGCTCTTTTTCATCTTGAGAGCTCTCGGATTCATTTCTGTGCTGGAACTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGAGCTTCTTCTACCACTGTGCTGACAGCATGAATTTGAGATT 601
QY 161 GlyIleAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
DB 602 GGAGGGCTCTTACTTGGGCAATTATTTCTTCCCTGTCTCCCTGATAGCTGATCATC 661
QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
DB 662 CTCGCTTTTCCCTGCTCATCTCCAGAGAAATCGCTCCAACTACATACATGCTTCAAGCC 721
QY 201 GluProLeuAlaThrArgSerSerProArgProGlyGluProProLysValLysSerGlu 220
DB 722 CAACCTTGTCCACAGAGAGCTCTCCAGGCTGTGATCACTCCAAAGTCAAGATGAG 781
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
DB 782 TTCAATTCTACAGCTCAGGCTGATGTG 811

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RESULT 6

US-10-063-547-79
Sequence 79, Application US/10063547
Publication No. US20020182638A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerilsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-547-79

Alignment Scores:

Pred. No.:	2,43e-131	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13	Indels:	0
DB:	13	Gaps:	0

US-09-787-677a-3 (1-230) x US-10-063-547-79 (1-1475)

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QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuGly 20
DB 122 ATGGCTCTCTTGGCTCCCACTTGCGCTACATCTTAGCGCTTCTGGGGCTTTGGG 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLySerTherSerTrpValGlyAlaSerIle 40
DB 182 ACCTGCTGTCCTGCTGCTCCCACTGGAAGAAACAGTTCTTAATGCGGTGCACGATT 241
QY 41 ValThrAlaValGlyPheSerTrpGlyLeuTrpMetGlyCysAlaThrHisSerThnGly 60
DB 242 GTACACGACATTGGCTTCTTCCAGGGCTCTGATGGAATGTGCCACACACAGCAGGC 301

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QY 61 IIEThGInGySaAppliEtyrSerThrLeuEngIyLeuProAlaAppliEgInAlaAla 80
DB 302 ATACCCAGGTGACATCTATAGACACCTTCTGGGCGCTGCGGTGACATCCAGGCTGCC 361
QY 81 G1AlaMetMetVal1ThrSerSerAla1SerSerLeuAlaCyS1Ile1SerVal1 100
DB 362 CAGGCCATGATGGAGACATCCAGGCAATCTCCCTGGCGCTGATTAATCTCTGTGTG 421
QY 101 GlyMetArgCyThrVal1PheCyGInGInSerArgAla1yAspArgVal1AlaVal1Ala 120
DB 422 GGCATGAGATGACACAGTCTTCTGCGCAAGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCA 481
QY 121 G1yG1yVal1PhePheIleLeuG1yG1yLeuEngIyPheIleProVal1AlaTPAsnLeu 140
DB 482 GGTGAGATCTTTTTCATCTTGAGGCGCTCTGGAGATTCATCTGTTGCTGGAAATCTT 541
QY 141 H1eG1y1IleLeuArgAspPheTySerProLeuVal1ProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGGACTTCTACTCACACTGCTGCTGACATGAAATTTGAGATT 601
QY 161 G1yG1uAlaLeuTyrlLeuG1y1Ile1SerSerLeuPheSerLeuIleAlaG1y1Ile 180
DB 602 GGAAGAGGCTCTTACTTGGGCAATATTCTTCCCTGTTCTCCGTAGATGCTGAATCATC 661
QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntyTyrrAspAlaTyrglnAla 200
DB 662 CTCTGCTTTTCCGCTCATCCAGAGAAATGCTCCAACTACATACGATGCTTACCAAGCC 721
QY 201 G1nProLeuAlaThrArgSerSerProArgProG1yGlnProPolysVal1ySerGlu 220
DB 722 CAACCTTTGCCACAGAGAGCTCTCCAGGCTGTGCACTCCCAAGTCAAGAGTGA 781
QY 221 PheAsnSerTySerLeuThrG1yTyrrVal 230
DB 782 TTCATATCTTACAGCTGACAGGCTATGTG 811

RESULT 7

US-10-063-551-79
; Sequence 79, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-79

Alignment Scores:

Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-787-677A-3 (1-230) X US-10-063-551-79 (1-1475)

QY 1 MetAlaSerLeuG1yLeuG1nLeuVal1G1yTyrr1IleuEngIyLeuLeuG1y 20
DB 122 ATGGCTCTTCTTGGCTTCACTTATGAGGCTTACATCTTACGCTTCTTGGGCTTTTGGG 181
QY 21 ThrLeuVal1AlaMetLeuLeuProSerTrpLysThrSerSerTyrrVal1yAlaSerIle 40
DB 182 ACATGGTTCCATGCTGCTCCAGGTGAGAAAACAAGTCTTATGTCGGTGCAGCATT 241
QY 41 Val1ThrAlaVal1G1yPheSerLysG1yLeuTyrrMetG1yCyVal1AlaThrHisSerThnGly 60
DB 242 GTGACAGACATTTGCTTCTCCAGGCGCTTGATGAAATGTGCCACACACAGCAGG 301
QY 61 IIEThGInGySaAppliEtyrSerThrLeuEngIyLeuProAlaAppliEgInAlaAla 80
DB 302 ATACCCAGGTGACATCTATAGACACCTTCTGGGCGCTGCGGTGACATCCAGGCTGCC 361
QY 81 G1nAlaMetMetVal1ThrSerSerAla1SerSerLeuAlaCyS1Ile1SerVal1 100
DB 362 CAGGCCATGATGGAGACATCCAGGCAATCTCCCTGGCGCTGATTAATCTCTGTGTG 421
QY 101 GlyMetArgCyThrVal1PheCyGInGInSerArgAla1yAspArgVal1AlaVal1Ala 120
DB 422 GGCATGAGATGACACAGTCTTCTGCGCAAGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCA 481
QY 121 G1yG1yVal1PhePheIleLeuG1yG1yLeuEngIyPheIleProVal1AlaTPAsnLeu 140
DB 482 GGTGAGATCTTTTTCATCTTGAGGCGCTCTGGAGATTCATCTGTTGCTGGAAATCTT 541
QY 141 H1eG1y1IleLeuArgAspPheTySerProLeuVal1ProAspSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGGACTTCTACTCACACTGCTGCTGACATGAAATTTGAGATT 601
QY 161 G1yG1uAlaLeuTyrlLeuG1y1Ile1SerSerLeuPheSerLeuIleAlaG1y1Ile 180
DB 602 GGAAGAGGCTCTTACTTGGGCAATATTCTTCCCTGTTCTCCGTAGATGCTGAATCATC 661
QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntyTyrrAspAlaTyrglnAla 200
DB 662 CTCTGCTTTTCCGCTCATCCAGAGAAATGCTCCAACTACATACGATGCTTACCAAGCC 721
QY 201 G1nProLeuAlaThrArgSerSerProArgProG1yGlnProPolysVal1ySerGlu 220
DB 722 CAACCTTTGCCACAGAGAGCTCTCCAGGCTGTGCACTCCCAAGTCAAGAGTGA 781
QY 221 PheAsnSerTySerLeuThrG1yTyrrVal 230
DB 782 TTCATATCTTACAGCTGACAGGCTATGTG 811

RESULT 8

US-10-028-072-491
; Sequence 491, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028, 072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
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PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770

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PRIOR APPLICATION NUMBER: 60/069212
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PRIOR APPLICATION NUMBER: 60/073612
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PRIOR FILING DATE: 1998-02-09
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PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
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PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
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PRIOR FILING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
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PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Alignment Scores:

Pred. No.:	2,436-131	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-787-677a-3 (1-230) x US-10-028-072-491 (1-1475)

Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGCCCTCCACCTTGCGCTACATCTTAGGCTTTGGGGCTTTGGGC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
Db 182 ACACTGGTTCGACGCTGCTCCAGCTGGAAAACAACTTATATGTCGGTCCAGCATTT 241
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGATTGGCTTCTCCAAAGGCTCTGATGGAATGTGCACACACAGCAGGC 301
Qy 61 IleThrGlnCysAspIleTySerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCAACCCAGGTGACATCTATAGCACTTCTGGGCTTGGCCGCTGACATCAGGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGAGATCATCCAGTCAATCTCCCTCGGCTGCATTATCTGTGGTG 421
Qy 101 GlyMetArgCysTrpValPheCysGlnGlySerArgAlaValAspAlaValAla 120
Db 422 GGCAATGAGATGACAGTCTTCTCCAGGAATCCGAGCAAAAGACAGTGGCGGTAGCA 481
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGAGATCTTTTCACTCTTGAGGCTCTCGGATTCATCTCGTGGCTGGAACTTT 541
Qy 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGluIle 160

Db 542 CATGGATCTTACGGGACTTCTACTACACACATGTCCTGACAGCATGAATTTGAGATT 601
Qy 161 GlyAlaAlaLeuTyTrpLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAAGGCTCTTTACTTGGGCAATTATTTCTCTGTTCTCCCTGATAGCTGGAATCATC 661
Qy 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyTrpAspAlaTyGlnAla 200
Db 662 CTCTGCTTTCCGCTCATCTCCAGAAATCGCTCCAACTACATACATGCTCCAAAGCC 721
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
Db 722 CAACCTCTTCCCAAGAGACTCTCCAAAGGCTGTGTCACCTCCAAAGTCAAGAGTAG 781
Qy 221 PheAsnSerTySerLeuThrGlyTyTrpVal 230
Db 782 TTCATTTCTTACAGCTCTGACAGGAGGTATGTT 811

RESULT 9

US-10-063-616-79
Sequence 79, Application US/10063616
Publication No. US20030013855A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Paim
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-616-79

Alignment Scores:

Pred. No.:	2,436-131	Length:	1475
Score:	1174.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-787-677a-3 (1-230) x US-10-063-616-79 (1-1475)

Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGCCCTCCACCTTGCGCTACATCTTAGGCTTTGGGGCTTTGGGC 181
Qy 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
Db 182 ACACTGGTTCGACGCTGCTCCAGCTGGAAAACAACTTATATGTCGGTCCAGCATTT 241
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTrpMetGlyCysAlaThrHisSerThrGly 60
Db 242 GTGACACAGATTGGCTTCTCCAAAGGCTCTGATGGAATGTGCACACACAGCAGGC 301
Qy 61 IleThrGlnCysAspIleTySerThrLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCAACCCAGGTGACATCTATAGCACTTCTGGGCTTGGCCGCTGACATCAGGCTGCC 361
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100


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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-79

Alignment Scores:
Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-569-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGCCCTCCCACTGTGGCTACATCTCAGGCTTCTGGGCTTTTG3GC 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
Db 182 ACACGTGTTGCCATGCTGCTCCCACTGGAACCAAGTTCTTATGTCGGTCCAGCATT 241

QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrHisSerThyGly 60
Db 242 GTGACACAGCTGGCTTCTCCAGGCTCTGATGGAATGTGCACACAGCAGCAGGC 301

QY 61 IleThrGlnCysAspIleTySerThrLeuGlnGlyLeuProAlaAspIleGlnAlaAla 80
Db 302 ATACCCAGGTGACATCTATAGCACCTTCTGGGCTTCCGCTGACATCCAGGCTGCC 361

QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGATGATCATCCAGCATCTCCCTCCGCTGCATTAATCTGTG6TG 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATGAGATGCACAGCTTCTCCAGGAATCCGAGCNAAGACAGATGGCGGTAGCA 481

QY 121 GlyGlyValAlaPhePheIleLeuGlyGlyLeuGlnGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGAGACTCTTTTCATCTTGGAGGCTCTGAGGATTCATCTGTGGCTGGAATCTT 541

QY 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGlnIle 160
Db 542 CATGGATCTCAACGGACTTCTACTCACTGATGCTGACACAGCAATTTGAGATT 601

QY 161 GlyGlnAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAGAGGCTCTTACTTGGCATTAATTTCTCCCTGTTCTCCGATAGCTGGAATCATC 661

QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyTyTrpAspAlaTyGlnAla 200
Db 662 CTCGCTTTTCCGCTCATCCAGAGAAATGCTCCAACTACAGATGCTTACCAAGCC 721

QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGln 220
Db 722 CAACCTTTGCGCAACAGAGCTCTCCAAAGCTGTGCTCACTCCCAAGTCAAGAGTGA 781

QY 221 PheAsnSerTySerLeuThyGlyTyVal 230
Db 782 TTCAAATTCCTACAGCTGACAGGCTATGTG 811

RESULT 12
US-10-063-513-79
; Sequence 79, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William L.
; TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; PRIORITY FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-79

Alignment Scores:
Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-063-513-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 122 ATGGCCCTCTTGCCCTCCCACTGTGGCTACATCTCAGGCTTCTGGGCTTTTG3GC 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTyValGlyAlaSerIle 40
Db 182 ACACGTGTTGCCATGCTGCTCCCACTGGAACCAAGTTCTTATGTCGGTCCAGCATT 241

QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGlyCysAlaThrHisSerThyGly 60
Db 242 GTGACACAGCTGGCTTCTCCAGGCTCTGATGGAATGTGCACACAGCAGCAGGC 301

QY 61 IleThrGlnCysAspIleTySerThrLeuGlnGlyLeuProAlaAspIleGlnAlaAla 80
Db 302 ATACCCAGGTGACATCTATAGCACCTTCTGGGCTTCCGCTGACATCCAGGCTGCC 361

QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGATGATCATCCAGCATCTCCCTCCGCTGCATTAATCTGTG6TG 421

QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
Db 422 GGCATGAGATGCACAGCTTCTCCAGGAATCCGAGCNAAGACAGATGGCGGTAGCA 481

QY 121 GlyGlyValAlaPhePheIleLeuGlyGlyLeuGlnGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGAGACTCTTTTCATCTTGGAGGCTCTGAGGATTCATCTGTGGCTGGAATCTT 541

QY 141 HisGlyIleLeuArgAspPheTySerProLeuValProAspSerMetLysPheGlnIle 160
Db 542 CATGGATCTCAACGGACTTCTACTCACTGATGCTGACACAGCAATTTGAGATT 601

QY 161 GlyGlnAlaLeuTyLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GGAGAGGCTCTTACTTGGCATTAATTTCTCCCTGTTCTCCGATAGCTGGAATCATC 661

QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAsnTyTyTrpAspAlaTyGlnAla 200
Db 662 CTCGCTTTTCCGCTCATCCAGAGAAATGCTCCAACTACAGATGCTTACCAAGCC 721

QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGln 220
Db 722 CAACCTTTGCGCAACAGAGCTCTCCAAAGCTGTGCTCACTCCCAAGTCAAGAGTGA 781

QY 221 PheAsnSerTySerLeuThyGlyTyVal 230
Db 782 TTCAAATTCCTACAGCTGACAGGCTATGTG 811
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RESULT 13
US-10-063-515-79
; Sequence 79, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION: 2002-05-01
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-515-79

Alignment Scores:
Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-09-787-677a-3 (1-230) x US-10-063-515-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 122 ATGGCTCTCTTGGCTCCCAACTGTGGCTACATCTTAGGCTTGGGGCTTTTGGG 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTrpValGlyAlaSerIle 40
Db 182 ACCTGTTGCCATGCTGCTCCCAAGTGAAGAAAGTTCTTATGTCGGTGCAGCATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTACACGACGCTTGGCTTCTCCAGGGCTCTGATGAAATGTCACACACAGCAGC 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCAGGTGACATCTATACACCCCTCTGGGCTGCGCCGTCGATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGTGACATCCAGTGCATCTCTCCCTGCGCATTAATCTCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIlyAspArgValAlaValAla 120
Db 422 GCGATAGATGACACAGTCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGCGTGCA 481
QY 422 GCGATAGATGACACAGTCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGCGTGCA 481
QY 121 GlyIleValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 482 GGTGGAGTCTTTTCTTCTTCTTGGAGGCTCTGGGATTCATTCCTGTGCTGGAATCTT 541
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
Db 542 CATGGATCTCTTACGAGATCTTCTACCACTGGTGTCTTACAGCATGAATTTGAAATT 601
QY 161 GlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 602 GAGAGGCTCTTACTTGGGCAATTATTTCTCCCTGTCTCCTGATAGCTGAAATCATC 661
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RESULT 14
US-10-063-512-79
; Sequence 79, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION: 2002-05-01
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-79

Alignment Scores:
Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-09-787-677a-3 (1-230) x US-10-063-512-79 (1-1475)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 122 ATGGCTCTCTTGGCTCCCAACTGTGGCTACATCTTAGGCTTGGGGCTTTTGGG 181
QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTrpValGlyAlaSerIle 40
Db 182 ACCTGTTGCCATGCTGCTCCCAAGTGAAGAAAGTTCTTATGTCGGTGCAGCATT 241
QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThrGly 60
Db 242 GTACACGACGCTTGGCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGCGTGCA 301
QY 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 302 ATCACCAGGTGACATCTATACACCCCTCTGGGCTGCGCCGTCGATCCAGGCTGCC 361
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 362 CAGGCCATGATGTGACATCCAGTGCATCTCTCCCTGCGCATTAATCTCTGTGGTG 421
QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaIlyAspArgValAlaValAla 120
Db 422 GCGATAGATGACACAGTCTTCTCCAGGAATCCCGAGCCAAAGACAGAGTGGCGTGCA 481
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QY 121 G1YGIYVALPHEPHEILELEUGLYLEULEUGLYPHEHLEPROVALAATPPANLEU 140
DB 482 GGTGGAGCTCTTTCATCTTGAGAGCTCTGGGATTCATCTGTGGCTGGAAATCTT 541
QY 141 H1G1Y1LEUARGAPHEITYRSEPRoleuValProApSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGGACTTCTACTCACACTGGTGGCTGACAGCAAGAAATTGGATTT 601
QY 161 G1YGIU1ALEUTYRLEUGLY1LE1ESerSerleuPheSerleu1leaG1Y1le1le 180
DB 602 GAGAGGCTCTTACTGGGCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAAATCATC 661
QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntYrYrAspAlaTYrGlnAla 200
DB 662 CTCTGCTTTCTGCTCATCTCCAGAGAAATGCTCCAACTACAGATGCTTACCAAGCC 721
QY 201 G1NProleu1aThraArgSerSerProArgProG1Yg1NProProLysValLysSerGlu 220
DB 722 CAACCTCTTCCCAAGAGCTCTCCAAAGCTGTGTAACCTCCCAAGTCAAGATGAG 781
QY 221 PheAnsSerTYrSerLeuThrg1YrVal 230
DB 782 TTCATTCCTACAGCTGACAGGGGTATGTG 811

RESULT 15

US-10-121-049-491
; Sequence 491, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowksi, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; PRIORITY FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 550
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 491
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-121-049-491

Alignment Scores:

Pred. No.: 2,43e-131 Length: 1475
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-787-677a-3 (1-230) x US-10-121-049-491 (1-1475)

QY 1 MetAlaSerLeuG1YLeuGlnLeuValG1Yr1LeuG1YLeuLeuG1YLeuLeuG1Y 20
DB 122 ATGGCCTCTTGGCCTTCAACTGTGGGCTACATCCCAAGCCTTCTGGGCTTTGGGC 181

QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysThrSerSerTYrValG1YAlaSerIle 40
DB 182 ACATGGATCTTCCATCTGCTCTCCCACTGAGAAAACAAGTTCTTATGCTGGTCCAGATT 241
QY 41 ValThrAlaValG1YPheSerLysG1YLeuTrpMetGluCYaAlaThrH1SerThrg1Y 60
DB 242 GTGACAGCACTTGGCTTCTTCCAAAGGGCTCTGGATGGAATGTCCACACACACAGGC 301
QY 61 IleThrg1NcyAspIleTYrSerThrLeuLeuG1YLeuProAlaAspIleGlnAla 80
DB 302 ATCAACCAGGTGACATCTATACACCTTCTGGGCTTGGCCCTGATCATTCCAGGCTGCC 361
QY 81 G1AlaMetMetValThrSerSerAla1ESerSerleu1aCYs1le1ESerVal1 100
DB 362 CAGGCCATGATGTGATGATCATCTGATGATCTCTCTCTGCTGATATCTCTGTG 421
QY 101 G1YMetArgCYrThrValPheCYg1N1SerArgAlaLysAspArgValAlaValAla 120
DB 422 GGCATGATGACACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCA 481
QY 121 G1YGIYVALPHEPHEILELEUGLYG1YLeuLeuG1YPHEHLEPROVALAATPPANLEU 140
DB 482 GGTGGAGCTCTTTCATCTTGAGAGCTCTGGGATTCATCTCTGTGGCTGGAAATCTT 541
QY 141 H1G1Y1LEUARGAPHEITYRSEPRoleuValProApSerMetLysPheGluIle 160
DB 542 CATGGATCTTACGGGACTTCTACTCACACTGGTGGCTGACAGCAAGAAATTGGATTT 601
QY 161 G1YGIU1ALEUTYRLEUGLY1LE1ESerSerleuPheSerleu1leaG1Y1le1le 180
DB 602 GAGAGGCTCTTACTGGGCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAAATCATC 661
QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAntYrYrAspAlaTYrGlnAla 200
DB 662 CTCTGCTTTCTGCTCATCTCCAGAGAAATGCTCCAACTACAGATGCTTACCAAGCC 721
QY 201 G1NProleu1aThraArgSerSerProArgProG1Yg1NProProLysValLysSerGlu 220
DB 722 CAACCTCTTCCCAAGAGCTCTCCAAAGCTGTGTAACCTCCCAAGTCAAGATGAG 781
QY 221 PheAnsSerTYrSerLeuThrg1YrVal 230
DB 782 TTCATTCCTACAGCTGACAGGGGTATGTG 811

Search completed: December 20, 2004, 18:07:41
Job time : 550 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 20, 2004, 13:31:01 ; Search time 3199 Seconds
(without alignments)
2619.924 Million cell updates/sec

Title: US-09-787-677a-3

Perfect score: 1174
Sequence: 1 MASLGLVGLVILGLLGLG.....PGQPKVKEFNSYSLTGVV 230

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPTO.spool/US09787677/runat.20122004.132739.19443/app.query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdd -LIST=45
-NOCAIIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09787677@cgn2.1 1 3437@runat.20122004.132739.19443 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic3:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	693	9	AY400251 Homo sapi
2	1137	96.0	693	9	AY400252 Pan trogl
3	1099	93.6	786	8	BZ215522 CH230-416
4	1096	93.4	693	9	AY400253 Mus muscu
5	1096	93.4	2829	3	AK004990 Mus muscu
6	1029.5	87.7	822	4	BG386074 602455248
7	1017	86.6	724	4	BI100253 602885716
8	1017	86.6	761	5	BP445902 BP445902
9	1014	86.4	727	4	BI101652 602887470

10	1002	85.3	680	2	BE304667	BE304667 601105783
11	1002	85.3	728	4	BG325755	BG325755 602424466
12	994	84.7	752	6	CB952500	CB952500 AGENCOURT
13	976.5	83.2	978	4	BG164062	BG164062 602341087
14	965	82.2	777	4	BI102100	BI102100 602887847
15	962.5	82.0	945	2	BE513091	BE513091 601171545
16	961	81.9	768	4	BI102679	BI102679 602888236
17	950	80.9	946	2	BF789255	BF789255 602105156
18	948	80.7	729	7	CN793010	CN793010 4127966 B
19	938	79.9	707	7	CK836649	CK836649 4061487 B
20	925.5	78.8	808	6	CA469366	CA469366 AGENCOURT
21	917	78.1	884	6	CA469620	CA469620 AGENCOURT
22	916.5	78.1	750	2	AM475316	AM475316 un64402.Y
23	909.5	77.5	706	4	BI148156	BI148156 602912333
24	908	77.3	685	7	CK975368	CK975368 4106482 B
25	903	76.9	818	6	CA469360	CA469360 AGENCOURT
26	900.5	76.7	804	2	BF784189	BF784189 602108052
27	895	76.2	666	9	CE239984	CE239984 L19T-988-
28	880	75.0	704	4	BI330754	BI330754 6029882419
29	875.5	74.6	754	4	BG972599	BG972599 602841188
30	869	74.0	648	7	CN788131	CN788131 4122426 B
31	868	73.9	836	6	CA492032	CA492032 AGENCOURT
32	865	73.7	650	7	CR546700	CR546700 DXFZp470L
33	865	73.7	652	7	CR628947	CR628947 DXFZp469L
34	862	73.4	774	7	CK031415	CK031415 AGENCOURT
35	861	73.3	1114	2	BF789836	BF789836 602105395
36	859	73.2	787	2	BF781962	BF781962 602106220
37	854	72.7	673	1	AI746723	AI746723 u106109.Y
38	843	71.8	643	3	BG328625	BG328625 602427889
39	838	71.4	678	5	BP138412	BP138412 BP138412
40	832	70.9	659	1	AI789490	AI789490 uK99h03.Y
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42	778.5	66.3	738	6	CA467958	CA467958 AGENCOURT
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44	770	65.6	496	6	CA885318	CA885318 B0117504
45	759.5	64.7	892	2	BF781303	BF781303 602106979

ALIGNMENTS

RESULT 1
AY400251
LOCUS
DEFINITION Homo sapiens CLDN2 gene, 693 bp DNA linear GSS 15-DEC-2003
ACCESSION AY400251
VERSION AY400251.1 GI:39756240
KEYWORDS GSS.

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
1 (bases 1 to 693)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL
PUBMED 14671302
2 (bases 1 to 693)

REFERENCE

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

TITLE

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source location/Qualifiers
1..693

gene /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="CLDN2"
/locus_tag="HCM0495"

ORIGIN

Alignment Scores:

Pred. No.: 2,77e-122 Length: 693
Score: 1174.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-787-677A-3 (1-230) x AY400251 (1-693)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 1 ATGGCCCTCTTGGCCCTCACTTGTGGCTACATCCCTGAGCTTCTGGGCTTTGGGC 60
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerTyrValGlyAlaSerIle 40
Db 61 ACACTGTTGCATGCTGCTCCAGCTGGAAAACAATTCTTATGTGGGTCCAGCATT 120
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaIleThrHisSerThGly 60
Db 121 GTGACACAGTGGCTCTCCAGGGCTCTGATGGAATGTGCACACACAGCAGGC 180
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db 181 ATCAACCAAGTGTACATCTATAGCACCTTCTGGGCTTGCCTGACATCCAGGCTGCC 240
QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
Db 241 CAGGCCATGATGGAGATCATCAGTGAATCTCTCCCTGGCTGATATATCTGTGTGTG 300
QY 101 GlyMetArgCysThrValPheCysGlnGluSerIleAlaValAspArgValAlaValAla 120
Db 301 GGCATGATGATGACAGTCTTCTGACAGAAATCCGACAGCAAGAGTGGCGGTAGCA 360
QY 121 GlyGlyValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaIleProAspLeu 140
Db 361 GGTGGAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATCTCTGTTGCTGGAATCTT 420
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160
Db 421 CATGGGATCTCGAGGACTTCTACTCACTGATGCTGACAGCATGAATTTGAGATT 480
QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
Db 481 GGAAGAGCTCTTACTTGGGATATTTCTTCCCTGTTCTCCGATGAGATGATCATC 540
QY 181 LeuCysPheSerCysSerSerGlnArgAspArgSerAntTyrIleAspAlaTyrGlnAla 200
Db 541 CTCTGCTTTTCTCTCTATCCAGAGAAATGCTCCATCTACATCTGATGCTCAAGACC 600
QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProValValIleSerGlu 220
Db 601 CAACCTCTTGCCACAGAGCTCTCCAAAGGCTGTCACTCCCAAGTCAAGAGTGAAG 660
QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 661 TTCATTCTACACCTGACAGGGTATGTG 690

RESULT 2
AY400252 693 bp DNA linear GSS 15-DEC-2003
LOCUS Pan troglodytes CLDN2 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY400252
VERSION AY400252.1 GI:39756241

KEYWORDS GSS
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
AUTHORS 1 (bases 1 to 693)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302

JOURNAL PUBLISHED
REFERENCE 2 (bases 1 to 693)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
location/Qualifiers
1..693
source
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="CLDN2"
/locus_tag="HCM0495"

ORIGIN

Alignment Scores:

Pred. No.: 5.88e-117 Length: 693
Score: 1127.00 Matches: 222
Percent Similarity: 96.52% Conservative: 0
Best Local Similarity: 96.52% Mismatches: 8
Query Match: 96.00% Indels: 0
DB: 9 Gaps: 0

US-09-787-677A-3 (1-230) x AY400252 (1-693)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
Db 1 ATGGCCCTCTTGGCCCTCACTTGTGGCTACATCCCTGAGCTTCTGGGCTTTGGGC 60
QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerTyrValGlyAlaSerIle 40
Db 61 ACNNTGTTGCCATGCTGCTCCAGCTGGAAAACAATTCTTATGTGGGTCCAGCATT 120
QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGluCysAlaIleThrHisSerThGly 60
Db 61 ACNNTGTTGCCATGCTGCTCCAGCTGGAAAACAATTCTTATGTGGGTCCAGCATT 120
QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAlaAla 80
Db 121 GTGACACAGTGGCTCTCCAGGGCTCTGATGGAATGTGCACACACAGCAGGC 180
QY 121 GlyGlyValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaIleProAspLeu 140
Db 361 GGTGGAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATCTCTGTTGCTGGAATCTT 420
QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetCysPheGluIle 160

Db	Accession	Source	Length	Score
Db	421	CATGGATCTCAGGCACTTCTACTCACCACCTGGTGGCTGACACAGTAATTTGACATT	480	
Qy	161	GIYLALALEUITYRLEUGLYILELLESERSEULEPHESEULEALAGLYILELLE	180	
Db	481	GGAGAGGCTCTTTACTTGGGACATTAATTTCTTCCGTCTCCCTGATAGCTGGAATCATC	540	
Qy	181	LEUYPHESERCYSESERSEGLARASPARSERSEANTYTYRARPALATYGLIALA	200	
Db	541	CTTGCTCTTTCCTCTCATCTCCAGGAATGCTCCAACTACATGATGCTCCACCAAGCC	600	
Qy	201	GLNPROLEUALATNARGSERSEPROARGPROGLYGLNPROPOLYSVALYSESEGLN	220	
Db	601	CAACCTCTTGCCACAGAGCTCTCCAGAGCTGCTGCTCACTCTCCCAAGTCAAGATGAG	660	
Qy	221	PHENANSEPTYRSEULEUTHNGLYTYRVAL	230	
Db	661	TTCAATTCCTACAGCTGACAGGATGTG	690	
RESULT 3				
LOCUS	BZ215522	786 bp DNA linear GSS 11-OCT-2002		
DEFINITION	CH230-416N16_TV CHORI-230 Segment 2 Rattus norvegicus genomic clone			
ACCESSION	BZ215522			
VERSION	BZ215522.1	GI:23873880		
KEYWORDS	GSS.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
REFERENCE	1 (bases 1 to 786)			
AUTHORS	Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Frazer, C.M.			
TITLE	Rat BAC End Sequences from Library CHORI-230 MboI segment			
JOURNAL	Unpublished (1999)			
COMMENT	Other GSSs: CH230-416N16_TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pletier de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html Plate: 416 row: N column: 16 Seq primer: T7 Class: BAC ends. Location/Qualifiers 1..786 /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="BN/SsNHsd/MCM" /db_xref="taxon:10116" /clone="CH230-416N16" /sex="Female" /cell_type="Brain" /clone_lib="CHORI-230 Segment 2" /note="vector: pTRABAC1.3; Site_1: MboI; Site_2: MboI; CHORI-230 Rat (BN/SsNHsd/MCM) BAC library produced by Pletier de Jong"			

Best Local Similarity:	96.09%	Conservative:	10
Percent Local Similarity:	91.74%	Mismatches:	9
Query Match:	93.61%	Indels:	0
DB:	8	Gaps:	0
US-09-787A-3 (1-230) x B215522 (1-786)			
Oy	1	Meta1aSerLeuGlyLeuGlnLeuValAlGlyTyr11LeuGlyLeuLeuGlyLeuLeuGly	20
Db	59	ATGGCCCTCCCTGGAGCGTCCAACTGATGGCTACATCTTACAGCCCTTTGGGGCTATTAGGC	118
Oy	21	ThiruValAlaMetLeuLeuLeuProSerTyrPheThrSerSerTyrValAlaSerIle	40
Db	119	ACATCGATTGCCATGCTGCTCCCAACTGGAGCAAGATTCTTATGTTGGGCCAGCATTT	178
Oy	41	ValThirAlaValAlGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrHisSerThirGly	60
Db	179	GTGA CGGGGTGGCTTTTCCAAAGGCGCTTGATGGATGGTGCGACCCACAGCACTGGC	238
Oy	61	IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaAla	80
Db	239	ATCCACCAAGTGTGATCTTACAGTACTTTTATAGACTTCTGCTGACATCCAGAGCTGCC	298
Oy	81	GlnAlaMetValIleThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal	100
Db	299	CAGGCGCATGATGGAGCATCCAGAGCAATGCTTCGCGGCTGCATTAATCTCTGGGTG	358
Oy	101	GlyMetArGysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla	120
Db	359	GGCATGAGATCCACAGTCTTCTGCCAGGAATCTGAGCTAAGACAGAGTGGCTGTATG	418
Oy	121	GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrPheLeu	140
Db	419	GGTGGAGCTTTTTCATCCTTGGTGGTATCCTGGGTATTTATCCAGTGTCTGGCATCTT	478
Oy	141	HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle	160
Db	479	CACGGCATCTCCGGAGCTTCTACTACCACTGTGTCCTGACACATGAAATTTGGATTT	538
Oy	161	GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle	180
Db	539	GGAGAGACTCTGTACTTGGGAATATATTTACAGCGCTTTTCTTGTAAGCTGGAGTATC	598
Oy	181	LeuCysPheSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla	200
Db	599	CTGCGCTTTCTGCTCACTCAGCAAGATGTATCAACTCATATGATGGCTACAGGCC	658
Oy	201	GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu	220
Db	659	CAGCCTCTTGGCATAGAGCTCTCCCAAGATCTGCTCAACAGCCCAAGCCMAAGTGAAG	718
Oy	221	PheAsnSerTyrSerLeuThrGlyTyrVal	230
Db	719	TTCAACTCATACAGCTGAGCTGGGTATGTG	748
RESULT 4	AY400253	693 bp	DNA linear
LOCUS	AY400253		
DEFINITION	Mus musculus CLDN2 gene, VIRIDAL TRANSCRIPT, partial sequence,		
ACCESSION	AY400253		
VERSION	AY400253.1		
KEYWORDS	SSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,D.R., Lu,F., Murphy,B.,		
	Todd,M.A., Tanenbaum,D.M., Civello,R., White,T.J., Sninsky,J.V.,		
	Adams,M.D. and Cargill,M.		
TITLE	Interfering nonneutral evolution from human-chimp-mouse orthologous		

JOURNAL	science	ciros	302	(5652)	1960-1963	(2003)
PUBMED	14671302					
REFERENCE	2	(bases	1	to	693)	
AUTHORS	Clark,A.G.,	Glancowski,S.,	Nielson,R.,	Thomas,P.,	Kejariwal,A.,	
	Todd,M.A.,	Tanenbaum,D.M.,	Civello,D.R.,	Lu,F.,	Murphy,B.,	
	Ferreira,S.,	Wang,G.,	Zheng,X.H.,	White,T.J.,	Sninsky,J.J.,	
	Adams,M.D.	and	Cargill,M.			
TITLE	Direct	Submission				
JOURNAL	Submitted	(16-NOV-2003)	Celera	Genomics,	45	West
	Rockville,	MD	20850,	USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.					
FEATURES	Location/Qualifiers					
source	1..693	/organism="Mus	musculus"			
	/mol_type="genomic	DNA"				
gene	/DB_xref="taxon:10090"					
	<1..>693					
	/gene="CLDN2"					
ORIGIN	/locus_tag="HCM0495"					
Alignment Scores:						
Pred. No.:	1..91e-113	Length:	693			
Score:	1096..00	Matches:	210			
Percent Similarity:	96..09%	Conservative:	11			
Best Local Similarity:	93..36%	Mismatches:	9			
Query Match:		Indels:	0			
DB:	9	Gaps:	0			
US-09-787-677A-3	(1-230)	x	AY40253	(1-693)		
QY	1	MeFA1SerLeuG1yLeuG1nLeuValG1Yr1LeuG1yLeuG1yLeuG1yLeuG1y	20			
Db	1	ATGGCTCCCTTGGCTGCTCCACTGGTGGGCTACACCTTAGGCTTTGGGCTTTAGGC	60			
QY	21	Th1eUvA1a1a1eUleUleUProSeRTp1yR1RSeSeTYrYvA1G1yA1Se1le	40			
Db	61	ACATCATTTGTCATGCTGCTGCCACCTGGCAACGAGTCTCTAGTTGGTGGCAGATT	120			
QY	41	ValTh1a1a1a1G1y1hSeSe1y1eU1eU1Pme1G1yC1bA1aTh1a1Se1Th1G1y	60			
Db	121	GTGACGGCGGTGGCTTTTCCAAAGGCTCTGGATGAGTGGCGACACACAGACAGGC	180			
QY	61	1leThG1nCySeAp1leTySeSeTh1eUleU1yLeuPro1aASe1leG1a1a1a	80			
Db	181	ATCACCCAGTGCATATCTACAGTACCTTTAGACCTTCCTGCTGCATCCAGGCTGCC	240			
QY	81	G1a1a1eU1eU1a1Th1SeSeSe1a1a1eSeSeSe1eU1a1CyA1e1leSeSeVal1a1	100			
Db	241	CAGGCATATGATGGTACGTCACAGTGAAGTCTCGTGGCTTGATATATCTGTGGTG	300			
QY	101	G1yMe1a1GSeTh1a1a1hCySeG1nG1uSe1a1a1y1bA1p1a1a1a1a1a1a1a	120			
Db	301	GGCATAGAGACACCGCTGTTCCAGAGATTTCCAGCTTAAGAGACAGTGGCTGATG	360			
QY	121	G1yG1yVal1p1hSe1leUleU1yG1yLeuG1yP1h1e1ProVal1a1a1a1a1a1a1a	140			
Db	361	GGTGGAGTCTTTTCACTCTGTTGGTGCATCTCGGCTTTATCCAGTTGCTTGAACTTT	420			
QY	141	H1eG1y1leU1a1R1p1hTySeSe1Pro1eU1a1ProA1pSeSe1y1p1hG1u1le	160			
Db	421	CATGGCATCTTGGGATCTTACTGCGCGTGGTTCCGACAGCATGAATTTGAATTT	480			
QY	161	G1yG1u1a1a1eU1y1r1eU1y1le1le1SeSeSe1eU1p1hSeSe1eU1a1a1G1y1le1le	180			
Db	481	GGAGAGGCTCTGACTTGGACATCACTCAGCCGTTTTCTTTGGTAGCGGAGTATC	540			
QY	181	LeU1Cy1p1hSeSe1ySeSeSeG1n1a1a1e1a1a1a1a1a1a1a1a1a1a1a1a1a	200			
Db	541	CTTTGCTTTTCCGCTCGCCCAAGGCAATCTGACCACTACTATGATGGCTTACAGGCC	600			

Oy	201	Gl1nPr0b1eM1aT1R1A1G1S1S1e1P1R1O1A1G1P1R1C1G1Y1I1n1P1R1O1L1Y1S1V1a1L1Y1S1e1G1U1	220
Db	601	CAGCCTTTCGCTACAGAGCTCTCCAGAGTCGTCTACAGCCCAAGCCACAGAGTGAG	660
Oy	221	PhenAmSerTYrSerLeuThrnglyTYrVal	230
Db	661	TTCAACTCATACAGCCTGACTGGGTATGTG	690
RESULT 5			
AK004990		2829 bp	RNA
LOCUS			linear
DEFINITION			HTC 03-APR-2004
ACCESSION			Mus musculus adult male liver cDNA, RIKEN full-length enriched
VERSION			library, clone:1300013G06 product:claudin 2, full insert sequence.
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
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[illegible]

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4583675"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_11b="N1H_MGC_15"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2
ECOR1; cDNA made by oligo-dT priming. Directionally

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cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) "

ORIGIN

Alignment Scores:

Pred. No.:	8,34e-106	Length:	822
Score:	1029.50	Matches:	215
Percent Similarity:	93.91%	Conservative:	1
Best Local Similarity:	93.48%	Mismatches:	13
Query Match:	87.69%	Indels:	3
DB:	4	Gaps:	1

US-09-787-677a-3 (1-230) x BG386074 (1-822)

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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGly 20
Db 127 ATGGCCCTCTTGCCCTCCAACTGTGGGCTACATCTAGGCTTCTGGGCTTTGGGC 186
Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrThrSerTyrValGlyAlaSerIle 40
Db 187 ACACTGGTGCACATGCTGCTCCAGCTGGAACAAAGTTCTTATGTGGTGCACGACT 246
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaThrHisSerThrGly 60
Db 247 GTGACACAGTGGCTTCTCCAGAGGCTCTGAGTGAATGTGCACACAGCAGCAGGC 306
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 307 ATACCCAGTGTGACATCTAATAGCACCCCTTGGGCTGCGCTGACATCCAGCTGCC 366
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 367 CAGGCCATGATGAGACATCAGTCAATCTCCCTGGCTGCATTAATCTCTGTGTG 426
Qy 101 GlnMetArgCysThrValPheCysGlnGlnSerArgAlaValAspArgValAlaValAla 120
Db 427 GGCATGAGATGACAGTCTTCTGCGAGAAATCCGAGCAAGAGTGGCGGTAGCA 486
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
Db 487 GGTGAGATCTTTTTCATCTTGGAGGCTCTGGGATTCATCTCTGTGGCTGGAATCT 546
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
Db 547 CATGGATCTTACCGGACTTCTACTACCACTGTGTGCTGACACATGAATTTGAGATT 606
Qy 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
Db 607 GGAAGAGCTCTTATCTGGGCAATTAATTCCTGTTCTCTGATAGCTGGAGATCATC 666
Qy 181 LeuCyAspSerCysSerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
Db 667 CTCGCTTTTCTCTCATCCAGAAATGCTCC-AACTACTAGATGCTTACAAGCA 725
Qy 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProPolysValLysSerGlu 220
Db 726 AACTCT--TGCAACAGAGCTCTCCAGGCTGTGTCACACTCCAAAAGTCAGAGAGAG 782
Qy 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
Db 783 GTCCAATC-TACAACTGACGGGTTGTGTG 811

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RESULT 7
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LOCUS 60288571cfl1 NCI CGAP_kid14 Mus musculus cDNA clone IMAGE:5041370
DEFINITION 5', mRNA sequence.
ACCESSION BI100253
VERSION BI100253.1 GI:14551146

KEYWORDS

EST.
Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

NIH-MGC <http://mgc.nci.nih.gov/>.

ATTNORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaps-rc@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM1113 row: 0 column: 03

High quality sequence stop: 722.

Location/Qualifiers

FEATURES

source

1..724

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5041370"

/lab_host="DH10B (T1 phage-resistant)"

/clone_1lb="NCI CGAP_kid14"

/note="Organ: Kidney; Vector: pCMV-Sport6, Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.82e-104	Length:	724
Score:	1017.00	Matches:	205
Percent Similarity:	94.32%	Conservative:	11
Best Local Similarity:	89.52%	Mismatches:	11
Query Match:	86.63%	Indels:	3
DB:	4	Gaps:	0

US-09-787-677a-3 (1-230) x BI100253 (1-724)

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Qy 4 LeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGlyLeuLeuGlyTyrLeuVal 23
Db 36 TTGGGCTTCAACTGAGTGGCTACATCTAGGCTTTGGGCTGTGAGCAATCCATT 95
Qy 24 AlaMetLeuLeu-ProSerTyrThrSerSerTyrValGlyAlaSerIleValThrAl 43
Db 96 GCATGCTGCTTCCCACTMGCGGAAGAGATTCTTATGTTGTGTGCGCAGAT-GTGAAGGC 154
Qy 43 AlaGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThrGlyIleThrG 63
Db 155 GATTGGCTTTCCAGAGGCTCTGATGAGTGTGCACACAGCAGCAGGATCACCCA 214
Qy 63 nCyAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAlaIleGlnAla 83
Db 215 GTGCAATATACAGTACCTTTAGACTTCTGCGAATCCAGAGCTCCAGGCGCAT 274
Qy 83 tMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValAlaGlyMetAr 103
Db 275 GATGATACCTCAGATGATATGCTGCTGCTGTGATTAATCTCTGTGGGCAATGAG 334
Qy 103 gCyThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAlaGlyGly 123
Db 335 ATGACCGGTGTCGACGAGATTCTCAGCTAAGAGAGAGTGTAGTGGGTGAGT 394
Qy 123 lPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeuHisGly 143
Db 395 CTTTTCATCTTGGTGGCATCTGAGCTTTATCCAGTTGAGATCTTCATGGCAT 454

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QY 143 elenArGAspPheTYrSerProLeuValProAspSerMetLysPheGluIleGlyGluAl 163
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 QY 163 aleuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIleLeuCyph 183
 Db 515 TCTGTACTTGGGCATCATCTCAGCCCTGTTTCTTTGTGTAGCCGAGTCACTCTTGCTT 574
 QY 183 eSerCySerSerGlnArgAsnArgSerAntTYrTYrAspAlaTYrGlnAlaGln-ProL 203
 Db 575 TTCTCTCTCGCCCGAGGGCAATGTACCAACTACTATGATGAGCTACCGAGCCAGACTTC 634
 QY 203 euAlaThrArgSerSerProArgProGlyGlnProProlYsValLysSerGluPheAsn 223
 Db 635 TTCCCACTAGGAGCTCTCCAGATCTGCTCTCAACAGCCCAAGCAGAGTTCACACT 694
 QY 223 eTYrSerLeuThrGlyTYrVal 230
 Db 695 CATACAGCTGACTGGGTATGTG 717

RESULT 8
 BP445902 761 bp mRNA linear EST 30-DEC-2003
 LOCUS BP445902 full-length enriched swine cDNA library, adult liver Sus
 DEFINITION scrofa cDNA clone LVR010047F07 5', mRNA sequence.
 ACCESSION BP445902 GI:40435969
 VERSION BP445902.1
 KEYWORDS EST.
 SOURCE Sus scrofa
 ORGANISM Sus scrofa (pig)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 1 (bases 1 to 761)
 Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
 Okumura,N., Hamasima,N. and Awata,T.
 PEDF (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 Nucleic Acids Res. 32 (1), D484-D488 (2004)
 CONTACT: Hirohide Uenishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in
 Animal Genome Research Program (Japan) by National Institute of
 Agrobiological Sciences and STAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.
 Location/Qualifiers
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 liver"

ORIGIN
 Alignment Scores:
 Pred. No.: 1 95e-104 Length: 761
 Score: 1017.00 Matches: 199
 Percent Similarity: 97.60% Conservative: 4
 Best Local Similarity: 95.67% Mismatches: 5
 Query Match: 86.63% Indels: 0
 DB: 5 Gaps: 0

US-09-787-677a-3 (1-230) x BP445902 (1-761)
 QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTYrIleLeuGlyLeuLeuGly 20
 Db 138 ATGGCTCTCTCGGCTCCCAACTTGTAGGCTATCATCTTGGGCTTCTGGGC 197
 QY 21 ThrLeuValAlaMetLeuLeuProSerTPYrThrSerSerTYrValGlyAlaSerIle 40
 Db 198 ACCCTGTTGCCATGCTGCTCCACAGTGGCAGACAGATTCTTAAGTCGGGGCAGACATC 257
 QY 41 ValThrAlaValGlyPheSerIysGlyLeuTrpMetGluCysAlaThrHisSerTrngly 60
 Db 258 GTACCGGAGTGCGCTTCTCCAGGGCTCTGATGAGTGTCACAGACACACTGGC 317
 QY 61 IleThrGlnCysAspIleTYrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 Db 318 ATCACCAGTGTCATCTACAGACACAGACTGGGCTGCTGCTGACATCCAGGCTGCC 377
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 378 CAGGCCATGATGGTGAATCTAGCCCATCTCTCTTGAGCTGTATCATCACCGTGTG 437
 QY 101 GlyMetArgCysThrValPheCysGlnGluSerArgAlaLysAspArgValAlaValAla 120
 Db 438 GGCATCGGATGGACCGCTCTTCTCCAGAACTCTCGGCCAAGACAGAGTGGGTGTG 497
 QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTrpAsnLeu 140
 Db 498 GGTGAGTCTTCTTCTCTTGAGGCTCTGCTGCTTCATCCCGTGGTGAATCTT 557
 QY 141 HisGlyIleLeuArgAspPheTYrSerProLeuValProAspSerMetLysPheGluIle 160
 Db 558 CATGGATCTCTGGGACTTCTACTCCCTCGTGTCTGACGACAGAAATTTGAGATC 617
 QY 161 GlyGluAlaLeuTYrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 Db 618 GAGAGGCTCTCTACTTGGGCATCATTTCTCTCTTCTCTGATGAGTGGATCATC 677
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerAntTYrTYrAspAlaTYrGlnAla 200
 Db 678 CTCTGCTTTTCCGCCCACTGACAGAAATCGCTCAACTACTACATGACTATCAGGCC 737
 QY 201 GlnProLeuAlaThrArgSerSer 208
 Db 738 CAGCCCTCGCCACCCGAGCTCT 761

RESULT 9
 B1101652 727 bp mRNA linear EST 26-JUN-2001
 LOCUS B1101652
 DEFINITION 602867470F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042825
 5', mRNA sequence.
 ACCESSION B1101652
 VERSION B1101652.1 GI:14552545
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 727)
 NIH-WGC <http://wgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM1117 row: k column: 18
 High quality sequence stop: 722.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5042825"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NCI CGAP Kid14"
/note="Organ: Kidney; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP library." "

ORIGIN

Alignment Scores:

Pred. No.: 4.01e-104 Length: 727
Score: 1014.00 Matches: 194
Percent Similarity: 97.62% Conservative: 11
Best Local Similarity: 92.38% Mismatches: 5
Query Match: 86.37% Indels: 0
DB: 4 Gaps: 0

US-09-787-677a-3 (1-230) x B1101652 (1-727)

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Qy 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleuGlyLeuGlyLeuGly 20
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Qy 21 ThrLeuValAlaMetLeuLeuProSerTyrThrSerTyrValGlyAlaSerIle 40
Db 150 ACATCCATTCGCATGCGCTTCCCACTGGCGAAGCGATTCCTATGTTGGTCCAGCAT 209
Qy 41 ValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAlaThrHisSerThrGly 60
Db 210 GTGACGCGCGGTGGCTTTCCAGGCGCTTCGATGAGTGTGGACACACAGCAGCAGC 269
Qy 61 IleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
Db 270 ATCACCCAGGCGCATCTACAGTACGACCTTTTAGACTCTCTGCTGACATCAGGCTGCC 329
Qy 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
Db 330 CAGGCCATGATGAGTGCAGTCCAGTGCATGTCCTCGGCTTGATATCTGTGTGTG 389
Qy 101 GlyMetArgCysThrValPheCysGlnIleSerTyrGlnAlaValAlaValAla 120
Db 390 GGCATGAGATGACCGTGTCTCTGCCAGATTCCTGAGCTAAGACAGAGTGGCTGTAGTG 449
Qy 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaThrAspLeu 140
Db 450 GGTGGAGTCTTTTTCATCTCTGGTGCACTCTGGGCTTTATCCAGTTGCTTGGAACTTT 509
Qy 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIysPheGlnIle 160
Db 510 CATGGCATTCCTGGGACTTCTACTCGCGCTGTCTCTGACACATGAATTTGAGATT 569
Qy 161 GlyGlnAlaLeuTyrLeuGlyTlleSerSerLeuPheSerLeuIleAlaGlyTlleIle 180
Db 570 GGAAGGCTCTGTACTTGGGCACTCATCTCAAGCCCTGTTTCTTGGTAGCGAGTATC 629
Qy 181 LeuCyPheSerCysSerSerGlnArgAspArgSerAntTyrTyrAspAlaTyrGlnAla 200
Db 630 CTTTGTCTTCTCTGCGCCCAAGGCAATGTACCACTAATGATGCTTACCAAGGCC 689
Qy 201 GlnProLeuAlaThrArgSerSerProArg 210
Db 690 CAGGCTCTTGCCACTAGAGCTCTCCAAGA 719

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RESULT 10
BE304667
LOCUS BE304667 680 bp mRNA linear EST 13-JUL-2000
DEFINITION 601105783F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988309 5'

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

mRNA sequence.

BE304667
BE304667.1 GI:9176036

EST.
Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 680)

NIH-MGC http://mgc.nci.nih.gov/

Unpublished (1999)

Contact: Robert Straubeberg, Ph.D.

Email: cgaaps-r@mail.nih.gov

Tissue Procurement: ARCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov

plate: LICM77 row: f column: 22

High quality sequence start: 27

High quality sequence stop: 680.

FEATURES

source

1..680
Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2988309"

/issue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_1lb="NIH MGC 15"

/note="Organ: colon; Vector: pORF7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adapter: GGACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies) "

ORIGIN

Alignment Scores:

Pred. No.: 8.36e-103 Length: 680
Score: 1002.00 Matches: 195
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.35% Indels: 0
DB: 2 Gaps: 0

US-09-787-677a-3 (1-230) x BE304667 (1-680)

```

Qy 36 ValGlyAlaSerIleValThrAlaValGlyPheSerIleGlyLeuTyrMetGlyCysAla 55
Db 38 GTCGTCGCCAGCATTTGACAGCAGTGGCTTCTCCAGGCGCTTGATGAGTATGCGC 97
Qy 56 ThrHisSerThrGlyIleThrGlnCysAspIleTyrSerThrLeuLeuGlyLeuProAla 75
Db 98 ACACACGACGACGACGACGACGATGTGACATCTACGACCCCTTGGGCTGGCCGCT 157
Qy 76 AspIleGlnAlaIleGlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCys 95
Db 158 GACATCCAGGCTGCCGAGGCGATGATGATGATGATGATGATGATGATGATGATGATG 217
Qy 96 IleIleSerValValGlyMetArgCysThrValPheCysGlnIleSerArgAlaValAsp 115
Db 218 ATATATCTCTGTGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 277
Qy 116 ArgValAlaValAlaGlyGlyValPhePheIleLeuGlyLeuLeuGlyPheIlePro 135
Db 278 AGAGTGGCGGTGAGGATGAGTCTTTTTCATCTTGGAGGCTCCCGGATTCATTCCT 337
Qy 136 ValAlaThrPheLeuHisGlyIleLeuArgAspPheTyrSerProLeuValProAspSer 155

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DB 338 GTTGGCTGGAATCTTCATGGGATCTTCAGGAGCTTCTACTCAGCAGCTGGTCTGACAGC 397
 QY 156 MetLysPheGluIleGlyGluAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeu 175
 DB 398 ATGAAATTTGAGATTGGAGAGGCTCTTACTTGGGATTAATTTCTTCCTGTTCTCCCTG 457
 QY 176 IleAlaGlyIleIleLeuCyPheSerCySerSerGlnArgAsnArgSerArgTyrTyr 195
 DB 458 ATAGCTGGAAATCATCT 517
 QY 196 AASPATYrGlnAlaGlnProLeuAlaThrArgSerSerProArgProGlyGlnProPro 215
 DB 518 GATGCTTACCAAGCCCAAGCTCTTCCCAAGAGCTCTCAAGAGCTGATCACTCC 577
 QY 216 LysValLysSerGlnPheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 578 AAGTCAGAGTGAGTTCAATCTCTACAGCTGACAGGTATGTG 622

RESULT 11
 LOCUS BG325755 728 bp mRNA linear EST 27-FEB-2001
 DEFINITION 60242446F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4562273 5',
 mRNA sequence.
 BG325755
 ACCESSION BG325755.1 GI:13132179
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 728) http://mgc.nci.nih.gov/
 AUTHORS NIH-MGC
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaops-remail.nih.gov
 Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://lml.mcgill.ca/linl/linl.htm
 Plate: LLCM1274 row: d column: 18
 High quality sequence stop: 708.

FEATURES

source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4562273"
 /cissue_type="renal cell adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_14"
 /note="Organ: Kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA Synthesis Kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:
 Pred. No.: 9.2e-103 Length: 728
 Score: 1002.00 Matches: 218
 Percent Similarity: 95.22% Conservative: 1
 Best Local Similarity: 94.78% Mismatches: 10
 Query Match: 85.35% Indels: 6
 Gaps: 4

US-09-787-677a-3 (1-230) x BG325755 (1-728)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuLeuGly 20
 DB 30 ATGGCTCTCTTGGCTCCCAAGTGGGCTACATCTAGGCTTCTGGGGCT-ITGGGC 88
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheThrSerSerTyrValGlyAlaSerIle 40
 DB 89 ACACGTGGTCCAGTGGCTCCCGACGTGAGAAACAAAGTTCTTAGTGGGTGGACATT 148
 QY 41 ValThrAlaValAlaGlyPheSerIleGlyLeuTyrMetGluCyAlaThrHisSerThrGly 60
 DB 149 GTACAGAGAGTTGGCTTCTCCAAAGGCTCTTGATGGAATGTCCACACACAGAGGC 208
 QY 61 IleThrGlnCyAspIleTyrSerThrLeuLeuGlyLeuProAlaAspIleGlnAla 80
 DB 209 ATCACCAGGTGACATCTATACACCTCTGCGGCTGCGCCCTCAATCCAGGCTGCC 268
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerVal 100
 DB 269 CAGGCCATGATGGTGAATCAGTGCATCTCTCCCTGGCTGCAATATCTGTGGTG 328
 QY 101 GlyMetArgCyThrValPheCyGlnGlnSerArgAlaLysAspArgValAlaAla 120
 DB 329 GGCATGAGATGACACAGTCTTCTGCGAGAAATCCGAGCCAAAGAGTGGGGTGA 388
 QY 121 GlyIleValPhePheIleLeuGlyIleLeuGlyPheIleProValAlaTyrPheLeu 140
 DB 389 GGTGGAGTCTTTTTCATCTCTGGAGGCTCTGGAATTCATTCCTGTGCTGGAATCTT 448
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetLysPheGluIle 160
 DB 449 CATGGATCTCTACGGAGCTTCTACTCAACCTGTGCTGACAGCAATGAATTTGAGATT 508
 QY 161 GlyIleAlaLeuTyrPheGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIleIle 180
 DB 509 GGAGAGGCTCTTACTTGGGCAATATTTCTCTCTGCTGCTGATAGTGAATATATC 568
 QY 181 LeuCyPheSerCySerSerGlnArgAsnArgSerAsnTyrTyrAspAlaTyrGlnAla 200
 DB 569 CTCTGCTTTTCCGTCATCTCCAGAGAAATCGCTCCAACTACATGATCTACCAAGCCC 628
 QY 201 GlnProLeuAlaThrArgSerSerProArgProGlyGlnProProLysValLysSerGlu 220
 DB 629 AACTCT--TGACCAAGAGCTCTCAAGGCT-GGTCACT-CCCAAGTCAGAGAGTGA 683
 QY 221 PheAsnSerTyrSerLeuThrGlyTyrVal 230
 DB 684 TC-AATTCCTACAG-CTGACAGGTATGTG 711

RESULT 12
 LOCUS CB952500 752 bp mRNA linear EST 29-APR-2003
 DEFINITION AGENCOURT 13692613 NIH_MGC_176 Mus musculus cDNA clone
 IMAGE:30303557 5', mRNA sequence.
 CB952500
 ACCESSION CB952500.1 GI:30208619
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 752)
 NIH-MGC http://mgc.nci.nih.gov/
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaops-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 CDNA Library Preparation: Michael Brownstein Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: NDCR74 row: e column: 06
 High quality sequence stop: 586.
 Location/Qualifiers

FEATURES

SOURCE

1. 752
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30303557"
 /lab_host="DH10B (TI-phage-resistant)"
 /clone_id="NIH_MGC_176"
 /note="Organ: kidney; Vector: pDNR-LIB; Site 1: SfiI (ggcgatcgccgc); Site 2: SfiI (ggcgatcgccgc); cDNA made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGACAGATGCGCATTCAGCCGCG-3' and
 5'-ATTCTAGAGCCGAGCGCGCATG-3' (30'NM-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5 kb size fraction. Library created in the laboratory of M. Brownstein (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 7,76e-102 Length: 752
 Score: 994.00 Matches: 190
 Percent Similarity: 97.57% Conservative: 11
 Best Local Similarity: 92.23% Mismatches: 5
 Query Match: 84.67% Indels: 0
 DB: 6 Gaps: 0

US-09-787-677a-3 (1-230) x CB952500 (1-752)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGly 20
 DB 108 ATGGCCCTCCCTGGCTCCCACTGCTGAGCTACCTCTAGCCCTTTGGGCTGTAGGC 167
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysTrpSerSerTrpValGlyAlaSerTlle 40
 DB 168 ACATCCATTCGACGATGCTCTCCCACTGCGGAACGAGATTCCTATGTTGGCCAGCATTT 227
 QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThgLy 60
 DB 228 GTGACGGCGGTGGCTTTCCAGAGGCTCTCGATGAGTGTGCGACACAGACAGAGGC 287
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 DB 288 ATCACCAGTGCAGATCTACAGATCCCTTTAGACTTCTGCTGACATCCAGGCTGCC 347
 QY 81 GlnAlaMetMetValTrpSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 DB 348 CAGGCCATGATGGAGCTCCAGTCCAGTACATGCTCGCTGGCTTGTATATCTCTGTGGTG 407
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaLysAspArgValAlaValAla 120
 DB 408 GGCATGAGATGACACGATGCTCTGCGAGATTCCTGAGCTAAGACAGAGTGGCTGTAGT 467
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTrpAsnLeu 140
 DB 468 GGTGGAGTCTTTTTCATCTCTGTGGGCAATCTCGGCTTTATCCAGTTGCTTGAATCTT 527
 QY 141 HisGlyIleLeuAlaGlyAspPheTyrSerProLeuValProAspSerMetLysPheGlnIle 160
 DB 528 CATGGCATCTTCGGGACTTCTACTCGCGCTGTGTCTCTGACAGACAGAAATTTGAAGATT 587
 QY 161 GlyGlnAlaLeuTyrLeuGlyIleIleSerSerLeuPheSerLeuIleAlaGlyIle 180
 DB 588 GGAAGAGCTCTGTACTTGGGATCATCTCAGCCCTGTTTCTTGTGAGCGGAGTCAATC 647
 QY 181 LeuCyPheSerCysSerSerGlnArgAsnArgSerArgTyrTyrAspAlaTyrGlnAla 200
 DB 648 CTTTGTCTTTCTCTGCGCCCGAGGCAATGATCACTACTATGATGCTACACAGGCC 707

QY 201 GlnProLeuAlaThrArg 206
 DB 708 CAGCCTCTTCCCACTAGG 725

RESULT 13

BG164062 978 bp mRNA linear EST 06-FEB-2001
 LOCUS 602341087F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449212 5',
 DEFINITION mRNA sequence.

ACCESSION

VERSION BG164062.1 GI:12670765

KEYWORDS

SOURCE EST.

ORGANISM

Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 978)

NIH-MGC <http://imgc.ncbi.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgabds-rc@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LLM10232 row: m column: 21

High quality sequence stop: 689.

FEATURES

SOURCE

1. 978

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4449212"

/tissue="IMR90 (hypernephroma, cell line)"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_89"

/note="Organ: kidney; Vector: pCMV-Sport6; Site 1: NotI,

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.3 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.08e-99 Length: 978
 Score: 976.50 Matches: 218
 Percent Similarity: 93.99% Conservative: 1
 Best Local Similarity: 93.56% Mismatches: 9
 Query Match: 83.18% Indels: 9
 DB: 4 Gaps: 1

US-09-787-677a-3 (1-230) x BG164062 (1-978)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrTlleLeuGlyLeuLeuGly 20
 DB 25 ATGGCCCTCTTGGCTCCCACTGCTGAGCTACCTCTAGCCCTTTGGGCT-TTGGGC 83
 QY 21 ThrLeuValAlaMetLeuLeuProSerTrpLysTrpSerSerTrpValGlyAlaSerTlle 40
 DB 84 ACATGGTTCGACGATGCTCTCCCACTGCGGAACAGATTCCTATGTTGGGCTAGCATTT 143
 QY 41 ValThrAlaValGlyPheSerLysGlyLeuTrpMetGluCysAlaThrHisSerThgLy 60
 DB 144 GTGACGACATTTGGCTTCTCAGAGGCTCTGATGAGAAATGTGCGACACAGACAGAGGC 203
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 DB 204 ATCACCAGTGTACATCTATAGACACCTTCTGCGGCTGCGCTGATCAATCCAGGCTGCC 263

Qy	81	GIlnlaImetctValThSerserAlaIeserSerLeuAlaCyellIeserVal	100
Db	264	CAGGCGATGATGGTACATCCAGTCCATCTCTCCCTGGCTGCATTTATCTCTGTGGTG	323
Qy	101	GIyweCaGyvrthValPheCysGlnIuSerAraGAlaIyAspAraGAlaIaValAla	120
Db	324	GGCATGATGATCACAGTCTTCTGCGACAGAAATCCGACCAAGACAGAGTGGCGGTAGCA	383
Qy	121	GIyGIyValIphPhePheIleuGIyGIyLeuGIyPheIleProValAlaIraPheIleu	140
Db	384	GATGAGTCTTTTTCATCTTGGAGGCGCTCCGAGATTCATTCCTGTGGCTCGGAATCTT	443
Qy	141	HisGIyIleLeuAraGAspPheIyIserProLeuValIProAspSerMetIySpheGluIle	160
Db	444	CATGGAGATCTTAAGGGACTTCTACTACACACTGGTGGCTGACAGCATGAAATTTGAGATT	503
Qy	161	GIyGIyAlaIeU-TyrIleuGIyIleIleIeserIleuPheSerIleuIleAlaGIyIleI	180
Db	504	GGAGAGGCTCTTTTACTTGGGACTTATTTCTTCCGTGTTCTCCGATATGCGGATCAT	563
Qy	180	eLeuCyAspPheSerCysSer-SerGlnAraGAsnAraSerAsnTyrIraAspAlaIyGlnA	200
Db	564	CCTCGCTTTTCTCTCTCAATCCAGAGAAATCGCTC-AACACTACAGATGCTTAC----	618
Qy	200	IaGlnPro-LeuAlaIraGysSerSerProAraGProGIyGlnProProIyValIySer	219
Db	619	--AAGCCAACTCTGCAAAAGAGGCTCTCCAA--GCTGTGCAACCTCCAAAGSTCAAGAG-	673
Qy	220	GIuPheAsnSerIyIserLeuThGIyIyVal	230
Db	674	GAGTTCAATTCCTACAGGCCGACAGGGATGTG	706

	LOCUS	B1102100	777 bp	mRNA	linear	EST 26-JUN-2000
	DEFINITION	602897847p1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043251				
	ACCESSION	B1102100				
	VERSION	B1102100.1 GI:14552993				
	KEYWORDS	EST.				
	SOURCE	Mus musculus (house mouse)				
	ORGANISM	Mus musculus				
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 777) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
	AUTHORS	Contact: Robert Strausberg, Ph.D.				
	TITLE	Email: cgapbs@mai.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L1A1L118 row: m column: 12 High quality sequence stop: 749.				
FEATURES	source	Location/Qualifiers 1..777				

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
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/clone_lib="NCI CGAP_Kid15"
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.75 kb. Construct generated by Life Technologies. Note: this is a NCI CGAP Library."

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ORIGIN	
Alignment Scores:	
Pred. No.:	1.57e-98
Score:	965.00
Percent Similarity:	96.60%
Best Local Similarity:	89.81%
Query Match:	82.20%
DB:	4
Gaps: 0	
Length:	777
Matches:	185
Conservative:	14
Mismatches:	7
Indels:	0

QY	1	Met1aseerleuglyleuglnleuValGlyTyrilleuglyleuuglyleuugly	20
Db	153	ATGGCTCTCCCTGGCGTTCAACTGTGTGGGCTACACTCTAGGCCCTTTGGGGCTTTAGGC	212
QY	21	ThrlleuValAlaMetleuLeuProSerTTrpIysThrSerSerYrValGlyAlaSerlle	40
Db	213	ACATTCACATTGGCAAGCGCTTCCCACTGGGAACGAGTTCCTATGTTGGCCAGCATT	272
QY	41	ValThrlaValAlGlyPheSerIySGlyLeuTrpMetIuCySaIaTrpHlIseTThGly	60
Db	273	GTGACGGCGGTGGCTTTTCCAGGGCTCTCGATGAGTGTGTGGACACACAGCAGCGC	332
QY	61	IlleThrgIuCySaapIleYrSerThrleuuglyleuProAlaapIleGlnAla	80
Db	333	ATCACCGACGTGGATATCTACAGTACACCTTTTAGACTTCTCCTCGTGCATCCAGCGGCC	392
QY	81	GlnAlaMetMetValTrpSerSerAlaIleSerSerleuAlaCysIleIleSerValVal	100
Db	393	CAGGCCATGATGATGAGGTCTCAGACATGCTCCGTGGCTGTGATATCTCTGTGTG	452
QY	101	GlyMetArGcYThrValPheCysGlnIuSerArGAlaIuSaPaArGValAlaValAla	120
Db	453	GGCATGAGATGCACGAGTCTTCCGACAGATCTCTGACCTAAGACACAGATGGCTGTAGTG	512
QY	121	GlyGlyValPhePheIleleuGlyGlyLeuIleuglyPheIleProValAlaIleTrpAsnLeu	140
Db	513	GGTGAAGCTTTTTCATCTTGGGGGATCTCTGGCTTTATCCAGATGGCTTGGAACTT	572
QY	141	HisGlyIleleuArGAspPheYrSerProleuValProAspSerMetIysPheGlnIle	160
Db	573	CATGGCATCTCTGGGACCTTCTACTGCGCGCTGTCTCTGACAGCATGAATTTGAAATT	632
QY	161	GlyGlnAlaLeuYrleuGlyIleIleIseSerleuPheSerleuIleAlaGlyIleIle	180
Db	633	GGAGAGGCTCTGTACTTGGGCATCATCTACAGCCCTGTATCTATGTAGAGCCGGAGTCATC	692
QY	181	LeuCySpheSerCySaSerSerGlnArGAsnArSerSerAsnYrTrpAspAlaYrGlnAla	200
Db	693	CTTGTCTTTCTCTGCTGCGCCCGAGGCAATGATCCAACTCATGTAGTGGCTAAGAGCC	752
QY	201	GlnProleuAlaIleArG 206	
Db	753	CAGCTCTTGGCACTAGG 770	
RESULT 15			
BE513091			
LOCUS			
DEFINITION	601117545F01 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545171 5',	945 bp	mRNA
ACCESSION	BE513091		linear
VERSION	BE513091.1		EST 07-AUG-2000
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 945)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph. D.		

Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LICM41 row: 1 column: 12
 High quality sequence start: 36
 High quality sequence stop: 782.
 Location/Qualifiers

FEATURES

1..945
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3545171"
 /issue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1b="NIH MGC 15"
 /note="Organ: colon; Vector: POTB; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Alignment Scores:

Pred. No.: 3.96e-98 Length: 945
 Score: 962.50 Matches: 208
 Percent Similarity: 91.38% Conservative: 4
 Best Local Similarity: 89.66% Mismatches: 15
 Query Match: 81.98% Indels: 6
 DB: 2 Gaps: 1

US-09-787-677a-3 (1-230) x BE513091 (1-945)

QY 1 MetAlaSerLeuGlyLeuGlnLeuValGlyTyrIleLeuGlyLeuGlyLeuGly 20
 Db 187 ATGGCCCTCTTGCGCTCCCACTGTGGGCTACATCTTCTGGGGCTTTTGGC 246
 QY 21 ThrLeuValAlaMetLeuLeuProSerTyrPheSerTyrValGlyAlaSerIle 40
 Db 247 ACACCTGGTGGCATCTGCTCCCGAGCTGGAACCAAGTTTATGTCGGCCAGCAT 306
 QY 41 ValThrAlaValGlyPheSerIleGlyLeuTyrPheGlyCysAlaIleHisSerThrGly 60
 Db 307 GTGACACAGTGGCTTCTCCAGGCGCTCGATGGATGTGCCACACACAGCAGGC 366
 QY 61 IleThrGlnCysAspIleTyrSerThrLeuGlyLeuProAlaAspIleGlnAla 80
 Db 367 ATCACCCAGGTGACATCTATAGCACCTTCTGGGCTGCGCGTGCATCCAGCTGCC 426
 QY 81 GlnAlaMetMetValThrSerSerAlaIleSerSerLeuAlaCysIleIleSerValVal 100
 Db 427 CAGGCCATGATGTGACATCCAGTGCATCTCTCCCTGGCGCTGATTAATCTCTGTG 486
 QY 101 GlyMetArgCysThrValPheCysGlnGlnSerArgAlaValAspArgValAlaValAla 120
 Db 487 GGCATGAGATGCACAGCTTCTCGCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCA 546
 QY 121 GlyGlyValPhePheIleLeuGlyGlyLeuLeuGlyPheIleProValAlaTyrAsnLeu 140
 Db 547 GGTGGAGTCTT-TTCAATCTTGGAGGCTCTGGGATTCATCTCTGTGGAGATCTT 605
 QY 141 HisGlyIleLeuArgAspPheTyrSerProLeuValProAspSerMetIlePheGlu-I 160
 Db 606 CATGGGATCTTACCGGACTTCTACTCACCACCTGGTGCCTGACAGCATGAATTTGAAGAT 665
 QY 160 egiyglualaleuTyrleuGlyIleIleSerSerLeuPheSer-LeuIlealaglyIle 180

Db 666 TGGCAGAGGCTCTTACTTGGGCTTATTTCTTCCCTGTTCTCCCTGATAGCTGAATCA 725
 QY 180 le-leuCyapheSerCysSerSerGlnArgAsnArgSerAntTyrTyrAspAlaTyrGln 199
 Db 726 TTCTCTGCTTTCCTGCTCATCTCCAGAAATCGGTCCAACTACTACATGCTTACCA 785
 QY 200 -AlaGlnProLeuAlaThrArgSerSerProArgProGlyGlnProProIleValIle 219
 Db 786 GGGGCCACCTCTTGCACAGAGAGCTCTCCAGGCGTTGGTCACTTCCCAAGCAAGA-- 843
 QY 219 rGluPheAsnSerTyrSerLeuThrGly 228
 Db 844 -GTGTTCAATCTTACAGCCTGACAGGG 870

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